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OM protein - protein search, using sw model

Run on: June 7, 2006, 05:43:07 ; Search time 51 Seconds
(without alignments)
919.930 Million cell updates/sec

Title: US-10-823-506-8

Perfect score: 2836
Sequence: 1 MAGAMTPPPVQPARPGF.....LPAKGEVQNALNDHGHRRH 536

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /EMC Celerra_sids3/prodata/2/iaa/5 COMB.pep:*

2: /EMC Celerra_sids3/prodata/2/iaa/6 COMB.pep:*

3: /EMC Celerra_sids3/prodata/2/iaa/7 COMB.pep:*

4: /EMC Celerra_sids3/prodata/2/iaa/H COMB.pep:*

5: /EMC Celerra_sids3/prodata/2/iaa/PCTUS COMB.pep:*

6: /EMC Celerra_sids3/prodata/2/iaa/RE COMB.pep:*

7: /EMC Celerra_sids3/prodata/2/iaa/backfilest1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2836	100.0	536	2 US-09-359-167-8	Sequence 8, Appli
2	2804.5	98.9	585	2 US-09-949-016-7705	Sequence 7705, Ap
3	2621	92.4	495	2 US-09-359-167-2	Sequence 2, Appli
4	2621	92.4	495	2 US-09-915-181A-7	Sequence 7, Appli
5	2329	82.1	495	2 US-09-359-167-4	Sequence 4, Appli
6	1698	59.9	495	2 US-09-359-167-10	Sequence 10, Appli
7	1698	59.9	495	2 US-09-359-167-12	Sequence 12, Appli
8	970	34.2	578	2 US-09-740-041-4	Sequence 4, Appli
9	970	34.2	582	2 US-09-915-181A-4	Sequence 4, Appli
10	955	33.7	585	2 US-09-740-041-2	Sequence 2, Appli
11	941	33.2	567	2 US-09-949-016-11354	Sequence 11354, A
12	940	33.1	560	1 US-08-647-484-2	Sequence 2, Appli
13	940	33.1	560	1 US-08-647-484-2	Sequence 2, Appli
14	940	33.1	560	1 US-08-430-033A-2	Sequence 2, Appli
15	940	33.1	560	1 PCT-US96-05792-2	Sequence 2, Appli
16	936	33.0	560	1 US-08-805-118-4	Sequence 4, Appli
17	936	33.0	560	1 US-09-391-958-4	Sequence 4, Appli
18	936	33.0	560	1 US-09-915-181A-5	Sequence 5, Appli
19	935	33.0	850	2 US-09-915-181A-3	Sequence 3, Appli
20	876	30.9	497	2 US-09-949-016-6616	Sequence 6616, Ap
21	810	28.6	552	2 US-09-270-767-45540	Sequence 45540, A
22	808	28.5	563	2 US-09-915-181A-6	Sequence 6, Appli
23	808	28.5	576	2 US-08-864-785-1	Sequence 1, Appli
24	806.5	28.4	465	2 US-09-915-181A-8	Sequence 8, Appli
25	801.5	28.3	467	1 US-08-805-118-3	Sequence 3, Appli
26	801.5	28.3	467	2 US-09-391-958-3	Sequence 3, Appli

27	793	28.0	480	1 US-08-724-394A-9	Sequence 9, Appli
28	686	24.2	436	2 US-09-949-016-11448	Sequence 11448, A
29	686	24.2	470	1 US-08-724-394A-10	Sequence 10, Appli
30	615.5	21.7	401	1 US-08-805-118-1	Sequence 1, Appli
31	615.5	21.7	401	2 US-09-391-958-1	Sequence 1, Appli
32	592.5	20.9	480	1 US-08-724-394A-11	Sequence 11, Appli
33	562	19.8	380	2 US-09-949-016-7053	Sequence 7053, Ap
34	453	16.0	460	2 US-09-489-039A-9663	Sequence 9663, Ap
35	445.5	15.7	234	2 US-09-270-767-45527	Sequence 45527, A
36	391	13.8	436	2 US-10-154-419-98	Sequence 98, Appli
37	387	13.6	438	2 US-10-154-419-95	Sequence 95, Appli
38	375	13.2	186	2 US-09-270-767-45384	Sequence 45384, A
39	373	13.2	434	2 US-09-489-039A-13633	Sequence 13633, A
40	370	13.0	470	2 US-09-328-352-6912	Sequence 6912, Ap
41	369	13.0	439	2 US-09-172-952-14	Sequence 14, Appli
42	369	13.0	439	2 US-09-922-501-12	Sequence 12, Appli
43	368	13.0	157	2 US-09-270-767-61037	Sequence 61037, A
44	355.5	12.5	455	2 US-09-489-039A-9942	Sequence 9942, Ap
45	347	12.2	204	2 US-10-104-047-2253	Sequence 2253, Ap

ALIGNMENTS

RESULT 1

US-09-359-167-8

Sequence 8, Application US/09359167

Patent No. 6803448

GENERAL INFORMATION:

APPLICANT: Hellerqvist, Carl

APPLICANT: Fu, Changlin

TITLE OF INVENTION: GBS Toxin Receptor

FILE REFERENCE: CARB-008/01US

CURRENT APPLICATION NUMBER: US/09/359,167

CURRENT FILING DATE: 1999-07-21

EARLIER APPLICATION NUMBER: 60-693,843

EARLIER FILING DATE: 1998-07-22

NUMBER OF SEQ ID NOS: 12

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 8

LENGTH: 536

TYPE: PRT

ORGANISM: Homo sapiens

US-09-359-167-8

Query Match 100.0%; Score 2836; DB 2; Length 536;
Best Local Similarity 100.0%; Pred. No. 5.6e-295;
Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MAGAMTPPPVQPARPGFGLSGRRSLCOVASTPAHVGVMSPVVDLARNDEESTDR	60
DB	1	MAGAMTPPPVQPARPGFGLSGRRSLCOVASTPAHVGVMSPVVDLARNDEESTDR	60
QY	61	TPLLPGARAEAPVCCSARYNLAIILAFGFFIVYALRWLSVALYDMVDSNTTLEENRT	120
DB	61	TPLLPGARAEAPVCCSARYNLAIILAFGFFIVYALRWLSVALYDMVDSNTTLEENRT	120
QY	121	SKACPEHSAPIKYHNNOTGKKYQMDAETQCMILGSPFYGIITIOIPCGYASKIGKMLL	180
DB	121	SKACPEHSAPIKYHNNOTGKKYQMDAETQCMILGSPFYGIITIOIPCGYASKIGKMLL	180
QY	181	GFGLIGRAVLTLPPIADIGVGPLYLRALBGLGSGVTPPAHAMSSNAAPLERSKL	240
DB	181	GFGLIGRAVLTLPPIADIGVGPLYLRALBGLGSGVTPPAHAMSSNAAPLERSKL	240
QY	241	SISYAGQLGTIVSLPSGIICVYMMWTVYFFFGTIGIFWFLMTLWVSDTQKHRIIS	300
DB	241	SISYAGQLGTIVSLPSGIICVYMMWTVYFFFGTIGIFWFLMTLWVSDTQKHRIIS	300
QY	301	HYEKYIILSLRNQLSQKSVPVVPLIKSLPLMAIVAHFSYMMFTYTLTLPTWKET	360
DB	301	HYEKYIILSLRNQLSQKSVPVVPLIKSLPLMAIVAHFSYMMFTYTLTLPTWKET	360

QY	361	LRFNVOENGFLSSLPYLGSLWLCMIITSGQAADNIRAKWNSTLCVRRI	FSLIGMIGPAVEL	420
Db	361	LRFNVOENGFLSSLPYLGSLWLCMIITSGQAADNIRAKWNSTLCVRRI	FSLIGMIGPAVEL	420
QY	421	VAAGTGTCYSLAVAFLTISTTTLGGCCSSGFSINHDIASVAGILLGINTPATI	PGMW	480
Db	421	VAAGTGTCYSLAVAFLTISTTTLGGCCSSGFSINHDIASVAGILLGINTPATI	PGMW	480
QY	481	GPVIAKSLTPDDTVGEMQTVFYAAAINVFGAIFPTLFAEGEONNALNDHGH	RRH	536
Db	481	GPVIAKSLTPDDTVGEMQTVFYAAAINVFGAIFPTLFAEGEONNALNDHGH	RRH	536

RESULT 2

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US-09-949-016-7705
; Sequence 7705, Application US/09949016
; Patent No. 6812139
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7705
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-7705

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Query Match 98.9%; Score 2804.5; DB 2; Length 585;

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Best Local Similarity 55.5%; Freq. NO. 1.0e-251;
Matches 534; Conservative 1; Mismatches 1; Indels 21; Gaps 1;

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QY      1  MAAGMT-----PRPQAPRGFGJSGRRSLLCVASTPAHV 39
      :
Db      29  MAAGASAPPLGAGTAGTRRGAVSSPPRPQAPRGFGJSGRRSLLCVASTPAHV 88
      :
QY      40  GVMRSVPRLARNDGESTDTRTLLGAPPAEAAAPCCSARNVLAIAFFGFVVALRV 99
      :
Db      89  GVMRSVPRLARNDGESTDTRTLLGAPPAEAAAPCCSARNVLAIAFFGFVVALRV 148
      :
QY      100 NISVALVDMVDSNTTLEDNRTSKACEBSAPIVAHNQTGKKYQMDAETGMLGSFFYG 155
      :
Db      149 NISVALVDMVDSNTTLEDNRTSKACEBSAPIKVNHNQTGKKYQMDAETGMLGSFFYG 208
      :
QY      160 YIITQPGGYVASKIGGKMLGSGIIGTAVLTFTPLAADLGVPILVLALEGLGCVT 219
      :
Db      209 YIITQPGGYVASKIGGKMLGSGIIGTAVLTFTPLAADLGVPILVLALEGLGCVT 268
      :
QY      220 PPAHAMMSWAPPLERSKULSISVGAQGTIVISPLSGIICYMMNTVVFYFFGTIGI 279
      :
Db      269 PPAHAMMSWAPPLERSKULSISVGAQGTIVISPLSGIICYMMNTVVFYFFGTIGI 328
      :
QY      280 PFFLLIMLWVSDTPQGHKRI SHEKEYIYSSLNNOSSQKSVWVWPLKSLPLMAIVAH 339
      :
Db      339 PFFLLIMLWVSDTPQGHKRI SHEKEYIYSSLNNOSSQKSVWVWPLKSLPLMAIVAH 388
      :
QY      340 FSYNNTFYLLTLPTYMKELILFNNVOENGLSSPLTGLSMLCMIISGQAADNIRAKNF 399
      :
Db      389 FSYNNTFYLLTLPTYMKELILFNNVOENGLSSPLTGLSMLCMIISGQAADNIRAKNF 448
      :
QY      400 STLCVARRISLIGMIGPAVFLVAGFICDYSLAVAFLLTISTTLGFCSSGFSINHLDA 459
      :
Db      449 STLCVARRISLIGMIGPAVFLVAGFICDYSLAVAFLLTISTTLGFCSSGFSINHLDA 508

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QY	460	PSVAGILILGTTNTPATIPGMNGSPVAKSLTDPNIVGEMQVFEYLAIAINFGALFFFLTA	519
Db	509	PSVAGILILGTTNTPATIPGMNGSPVAKSLTDPNIVGEMQVFEYLAIAINFGALFFFLTA	568
QY	520	KGEVQNMALNDHHGRH	536
Db	569	KGEVQNMALNDHHGRH	585

RESULT 3

```

US-09-359-167-2
; Sequence 2, Application US/09359167
; Patent NO. 6803448
; GENERAL INFORMATION:
; APPLICANT: Hellerqvist, Carl
; APPLICANT: Fu, Changlin
; TITLE OF INVENTION: GBS Toxin Receptor
; FILE REFERENCE: CARB-008/01US
; CURRENT APPLICATION NUMBER: US/09/359,167
; CURRENT FILING DATE: 1999-07-21
; EARLIER APPLICATION NUMBER: 60-693,843
; EARLIER FILING DATE: 1998-07-22
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: ParentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 495
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-359-167-2

```

Query Match 92.4%; Score 2621; DB 2; Length 495;

```
Best Local Similality 100.00; Freq. NO. 3.0e-2/2;
Matches 495; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY	42	MSBPVMDIARNQSEESTDTPLLPGAPAPBAAPVCCSARXVALTLAEFFGPIVYALRVNL	101
Db	1	MRSVVDLARNQSEESTDTPLLPGAPAPBAAPVCCSARXVALTLAEFFGPIVYALRVNL	60
QY	102	SVALVMDVDSNTTLEBNRTSKAPCEHSAPIKVHNQTKGKYQMDAETQGMILGSFFGYI	161
Db	61	SVALVMDVDSNTTLEBNRTSKAPCEHSAPIKVHNQTKGKYQMDAETQGMILGSFFGYI	120
QY	162	ITQIPGGYVASKTGGMLLGFGILGTAVLTLFTPIADLGVGPLIVLRALGEGEYTFP	221
Db	121	ITQIPGGYVASKTGGMLLGFGILGTAVLTLFTPIADLGVGPLIVLRALGEGEYTFP	180
QY	222	AMEAMSSMAPLERSKLTISYAGNOGTYSJPLSGIICYNNMTYVFVEFFGTGIFW	281
Db	181	AMEAMSSMAPLERSKLTISYAGNOGTYSJPLSGIICYNNMTYVFVEFFGTGIFW	240
QY	282	FLIMLWVSDTPQKHKRISHYEKEYIISLRNQUSQKSVBPVILKSLPLMAIVAHFS	341
Db	241	FLIMLWVSDTPQKHKRISHYEKEYIISLRNQUSQKSVBPVILKSLPLMAIVAHFS	300
QY	342	YNNFTFTLLTLPTWKEKILRENOENGLSLPYLGSWLCMIISGQAADNLRKXNFST	401
Db	301	YNNFTFTLLTLPTWKEKILRENOENGLSLPYLGSWLCMIISGQAADNLRKXNFST	360
QY	402	LCVRRIFSLIGMIGPAVFLVAAGFIGDCYSLAVAFLTISTTLGGFCSSGFSINHLDIAPS	461
Db	361	LCVRRIFSLIGMIGPAVFLVAAGFIGDCYSLAVAFLTISTTLGGFCSSGFSINHLDIAPS	420
QY	462	YAGILGINTPTATITGCMGVPIASLPDNTVGSQMOWFYIAAIVNFGAIFFTLPAKG	521
Db	421	YAGILGINTPTATITGCMGVPIASLPDNTVGSQMOWFYIAAIVNFGAIFFTLPAKG	480
QY	522	EVQNMALNDHHGHRH 536	
Db	481	EVQNMALNDHHGHRH 495	
RESULT	4		

RESULT 4


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Query Match      59.9%; Score 1698; DB 2; Length 495;
Best Local Similarity 67.8%; Pred. No. 6.2e-173;
Matches 335; Conservative 0; Mismatches 159; Indels 0; Gaps 0;

QY 42 MRSPPVDLANDEESTDRTPLLPGAPRAEAPVCSARYNLA1LAFEGFEIVYALRVNL 101
DB 1 MXXPVDAXXXGEBEXXDRXXXXXXARXEXAPCCSARYNXXALXFFGFXXYXLLXVNL 60
QY 102 SVALVDMVDSNTTLEDRNRTSKACPEHSAPIKVHHNQTGKKYQMDAETQGMILGSPFYGYI 161
DB 61 XVXXVXMXDSXTTXDXNRKXSKCXEHSAPIKVVXXQTXGKXXWDATQGMILKXFFXGYI 120
QY 162 ITQIPGGYVASKIGKMLGFGILGTAVALTLFTPIADLGVGPLIVLRALGEGEVTPP 221
DB 121 ITXIPGGYVASKXGKXXLXGIXXXAXXTLFTPIAADXGKXXXXLXALEXLEGXTXP 180
QY 222 AMHAMSSWAPPLERSKLSISYAGQLGTVISLPLSGIICYYMNTVYVFFGTIGIFW 281
DB 181 AMHAMSSWAPPLERSKLSXIXYAGALGTIVSLPLSGIICYYMNTVYVFFXXFXKXGXW 240
QY 282 FLIMTLVSDTPQKHRIHYEKEYIILSSRNQSSQKVPWPVILKSLPLMAIVAHFS 341
DB 241 FXXMIXLVSTPXXHKKXXXXEKKXILSSLNQSSQKVPWXXXXKXLPMAXXVAXFS 300
QY 342 YNMTFTYTLTLPTYMKEILRFNVQENGFLSSLPYLGSMICMILSGQAADNLRANKNFST 401
DB 301 YNMTFTYTLXLLPTXMKXXLRFXKQENGFLSSXXPYLXXMILCGQAADNLRANKNFST 360
QY 402 LCVRIEFLIGMIGPAVFLVAAFGICDYSLAVAFLTISTTLGGFCSSGFSINHLDIAPS 461
DB 361 XVXXRFXSLIXMIGPXXFLXXXXXXGCDYXKXVFLXISTXLGFCSSGFSINHLDIAPS 420
QY 462 YAGILGINTPATITGMPGVIAKSLTPDNTVGEQVFIYIAAIVPFAIFFTLPFAGK 521
DB 421 YAGXLLGITNXPATITGMPGXPIKXSTPXTXGEMQXXFXAAXXKFGAIFFTLPFAGK 480
QY 522 EVONMALNDHGHGR 535
DB 481 EXONMXXDXHGXGR 494

RESULT 7
US-09-359-167-12
; Sequence 12; Application US/09359167
; Patent No. 6803448
; GENERAL INFORMATION:
; APPLICANT: Heileqvist, Carl
; APPLICANT: Fu, Changlin
; TITLE OF INVENTION: GBS Toxin Receptor
; FILE REFERENCE: CARB-006/01US
; CURRENT APPLICATION NUMBER: US/09/359,167
; CURRENT FILING DATE: 1999-07-21
; EARLIER APPLICATION NUMBER: 60-693,843
; EARLIER FILING DATE: 1998-07-22
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 12
; LENGTH: 495
; TYPE: PRT
; ORGANISM: Artificial Sequence
US-09-359-167-12

Query Match      59.9%; Score 1698; DB 2; Length 495;
Best Local Similarity 67.8%; Pred. No. 6.2e-173;
Matches 335; Conservative 0; Mismatches 159; Indels 0; Gaps 0;

QY 42 MRSPPVDLANDEESTDRTPLLPGAPRAEAPVCSARYNLA1LAFEGFEIVYALRVNL 101
DB 1 MXXPVDAXXXGEBEXXDRXXXXXXARXEXAPCCSARYNXXALXFFGFXXYXLLXVNL 60
QY 102 SVALVDMVDSNTTLEDRNRTSKACPEHSAPIKVHHNQTGKKYQMDAETQGMILGSPFYGYI 161
DB 61 XVXXVXMXDSXTTXDXNRKXSKCXEHSAPIKVVXXQTXGKXXWDATQGMILKXFFXGYI 120

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QY 162 ITQIPGGYVASKIGKMLGFGILGTAVALTLFTPIADLGVGPLIVLRALGEGEVTPP 221
DB 121 ITXIPGGYVASKXGKXXLXGIXXXAXXTLFTPIAADXGKXXXXLXALEXLEGXTXP 180
QY 222 AMHAMSSWAPPLERSKLSISYAGQLGTVISLPLSGIICYYMNTVYVFFGTIGIFW 281
DB 181 AMHAMSSWAPPLERSKLSXIXYAGALGTIVSLPLSGIICYYMNTVYVFFXXFXKXGXW 240
QY 282 FLIMTLVSDTPQKHRIHYEKEYIILSSRNQSSQKVPWPVILKSLPLMAIVAHFS 341
DB 241 FXXMIXLVSTPXXHKKXXXXEKKXILSSLNQSSQKVPWXXXXKXLPMAXXVAXFS 300
QY 342 YNMTFTYTLTLPTYMKEILRFNVQENGFLSSLPYLGSMICMILSGQAADNLRANKNFST 401
DB 301 YNMTFTYTLXLLPTXMKXXLRFXKQENGFLSSXXPYLXXMILCGQAADNLRANKNFST 360
QY 402 LCVRIEFLIGMIGPAVFLVAAFGICDYSLAVAFLTISTTLGGFCSSGFSINHLDIAPS 461
DB 361 XVXXRFXSLIXMIGPXXFLXXXXXXGCDYXKXVFLXISTXLGFCSSGFSINHLDIAPS 420
QY 462 YAGILGINTPATITGMPGVIAKSLTPDNTVGEQVFIYIAAIVPFAIFFTLPFAGK 521
DB 421 YAGXLLGITNXPATITGMPGXPIKXSTPXTXGEMQXXFXAAXXKFGAIFFTLPFAGK 480
QY 522 EVONMALNDHGHGR 535
DB 481 EXONMXXDXHGXGR 494

RESULT 8
US-09-740-041-4
; Sequence 4; Application US/09740041
; Patent No. 6562593
; GENERAL INFORMATION:
; APPLICANT: MERKULOV, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL001001
; CURRENT APPLICATION NUMBER: US/09/740,041
; CURRENT FILING DATE: 2000-12-20
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 578
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-740-041-4

Query Match      34.2%; Score 970; DB 2; Length 578;
Best Local Similarity 40.9%; Pred. No. 1e-94;
Matches 201; Conservative 93; Mismatches 165; Indels 32; Gaps 9;

QY 51 RNDGESTDRTPLLPGAP---RAEAPVC-GSA-----RYNLA1LAFEGFEIVYALRVNL 101
DB 33 KQDNRETIETLE--DGKPLEVPEKAPLDCCTCFGLPRRYIIAIMGSLGFCISFGICRNL 90
QY 102 SVALVDMVDSNTTLEDRNRTSKACPEHSAPIKVHHNQTGKKYQMDAETQGMILGSPFYGYI 161
DB 91 GVAIVDMVNNSTI---HRGKVIKEKA-----KFNWDPETVGMIHGSPFWGYI 135
QY 162 ITQIPGGYVASKIGKMLGFGILGTAVALTLFTPIADLGVGPLIVLRALGEGEVTPP 221
DB 136 ITQIPGGYVASKRANRVFGAAILTLSTLMLIPSAARHYGCIVTRILQGLVEGVTPP 195
QY 222 AMHAMSSWAPPLERSKLSISYAGQLGTVISLPLSGIICYYMNTVYVFFGTIGIFW 281
DB 196 ACHGISWNAAPPLERSRLATTSFCGSYAGAVIAMPLAGILVQYTGMSVFFYVYGSGMW 255
QY 282 FLIMTLVSDTPQKHRIHYEKEYIILSSRNQSSQKVPWPVILKSLPLMAIVAHFS 341
DB 256 YMFMLLVSYESPDKHPTITDEBRRIEESIGESANLLGMEKPKTWPARKFTTSMPIYAI 315

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TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CL001307
 CURRENT APPLICATION NUMBER: US/09/949,016
 CURRENT FILING DATE: 2000-04-14
 PRIOR APPLICATION NUMBER: 60/241,755
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/237,768
 PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: 60/231,498
 PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 207012
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 11354
 LENGTH: 567
 TYPE: PRT
 ORGANISM: Human
 US-09-949-016-11354

Query Match 33.2%; Score 941; DB 2; Length 567;
 Best Local Similarity 39.5%; Pred. No. 1.3e-91;
 Matches 193; Conservative 93; Mismatches 162; Indels 40; Gaps 8;

53 DGEESTDRT---PLLP-----GAPRAEAPVCCSARVNLALAFEPFIYVALRVNLVAL 105
 45 DGRPVTTQTRDPVPVDTCTGFLPR-----RYIALMSGGFCISFGIRCNLGVAI 94
 106 VDNVDSNTTLEDNRTSKACPEHSAPIVKHNQTKYQMDAEFOGMLGSEFFGYITTOI 165
 95 VSMVNNSTT-----HRGHHVVQKAO----FSMDPEVGLIHGSEFFMGYITVOI 139
 166 PGGVYVASKIGKMLGFGILGTAVLTLPPIADLGVPLIVLRALEGEVTFPAMHA 225
 140 PGGFICQKPAANRVFGPAIVATSTLNLIPSAARVHGCIVFRIILQGLVEGTVPAChG 199
 226 MMSWAPPLERSKLISVYGAOLGTVISLPLSGIICYYNMNTVYFFFGTIGIFWFLW 285
 200 IWSKMAPPLERSRLATTAFCGSYAGAVVAMPPLAGVLVOYSGMSVFFVYGSFGIFWFLW 259
 286 IWLVDTPQKHKRIKSHYEKEYI-----LSLRNQLSSQKSVPMVPLKSLPLMAIVAH 339
 260 LTVSYESPALHPISIEBERKIYEDAIAGESAKLMPPL-TKSTWRKRFFTSMFYAIIIVAN 318
 340 FSYNMFTFYTLTLPTMYKEILRFNVQENGFLSLPYLGSWLCMILSGQADNLRAKMF 399
 319 FCSWMTFYLLISOPAFEEVFGFEISKVGLVSLPHLWMTIIVPIGGQIADFLRSRIM 378
 400 STLCVRRIEFLIGMIGPAVFLVAAFGICDYSILAVALFJTISTLGGFCSSGFSINHLIDIA 459
 379 STTNVRRLKNNCGFGMEATILLVVGYSKSGVAISFLVALVGFSGFALISGFVNNHDDIA 437
 460 PSYAGILGTTNTPATIPGMVGVPIAKSLTPDNTVGMQVTFYIAAINVFGAIFFTLFA 519
 438 PRYASIMGISNGVGLISGWCPIIVGAMTKHKTREMOYVFLIASLVHVGIVIFGVFA 497
 520 KGEVQWMA 527
 498 SGEKQWMA 505

RESULT 12
 US-08-647-484-2
 Sequence 2, Application US/08647484
 Patent No. 5616677
 GENERAL INFORMATION:
 APPLICANT: NI, Binhui
 APPLICANT: Paul, Steven M.
 TITLE OF INVENTION: HUMAN BRAIN SODIUM DEPENDENT INORGANIC
 TITLE OF INVENTION: PHOSPHATE COTRANSPORTER AND RELATED NUCLEIC ACID COMPOUNDS
 NUMBER OF SEQUENCES: 3
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Eli Lilly and Company
 STREET: Lilly Corporate Center
 CITY: Indianapolis

STATE: Indiana
 COUNTRY: United States of America
 ZIP: 46285
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/647,484
 FILING DATE: 14-MAY-1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/430,033
 FILING DATE: 27-APR-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Gaylo, Paul J.
 REGISTRATION NUMBER: 36,808
 REFERENCE/DOCKET NUMBER: X-10006
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (317) 276-0756
 TELEFAX: (317) 276-3861
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 560 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-647-484-2

Query Match 33.1%; Score 940; DB 1; Length 560;
 Best Local Similarity 39.5%; Pred. No. 1.6e-91;
 Matches 193; Conservative 93; Mismatches 162; Indels 40; Gaps 8;

53 DGEESTDRT---PLLP-----GAPRAEAPVCCSARVNLALAFEPFIYVALRVNLVAL 105
 38 DGRPVTTQTRDPVPVDTCTGFLPR-----RYIALMSGGFCISFGIRCNLGVAI 87
 106 VDNVDSNTTLEDNRTSKACPEHSAPIKVHNQTKYQMDAEFOGMLGSEFFGYITTOI 165
 88 VSMVNNSTT-----HRGHHVVQKAO----FSMDPEVGLIHGSEFFMGYITVOI 132
 166 PGGVYVASKIGKMLGFGILGTAVLTLPPIADLGVPLIVLRALEGEVTFPAMHA 225
 133 PGGFICQKPAANRVFGPAIVATSTLNLIPSAARVHGCIVFRIILQGLVEGTVPAChG 192
 226 MMSWAPPLERSKLISVYGAOLGTVISLPLSGIICYYNMNTVYFFFGTIGIFWFLW 285
 193 IWSKMAPPLERSRLATTAFCGSYAGAVVAMPPLAGVLVOYSGMSVFFVYGSFGIFWFLW 252
 286 IWLVDTPQKHKRIKSHYEKEYI-----LSLRNQLSSQKSVPMVPLKSLPLMAIVAH 339
 253 LTVSYESPALHPISIEBERKIYEDAIAGESAKLMPPL-TKSTWRKRFFTSMFYAIIIVAN 311
 340 FSYNMFTFYTLTLPTMYKEILRFNVQENGFLSLPYLGSWLCMILSGQADNLRAKMF 399
 312 FCSWMTFYLLISOPAFEEVFGFEISKVGLVSLPHLWMTIIVPIGGQIADFLRSRIM 371
 400 STLCVRRIEFLIGMIGPAVFLVAAFGICDYSILAVALFJTISTLGGFCSSGFSINHLIDIA 459
 372 STTNVRRLKNNCGFGMEATILLVVGYSKSGVAISFLVALVGFSGFALISGFVNNHDDIA 430
 460 PSYAGILGTTNTPATIPGMVGVPIAKSLTPDNTVGMQVTFYIAAINVFGAIFFTLFA 519
 431 PRYASIMGISNGVGLISGWCPIIVGAMTKHKTREMOYVFLIASLVHVGIVIFGVFA 490
 520 KGEVQWMA 527
 491 SGEKQWMA 498

RESULT 13
 US-08-647-481-2

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; Sequence 2, Application US/08647481
; Patent No. 5618918
; GENERAL INFORMATION:
; APPLICANT: Ni, Binhui
; TITLE OF INVENTION: HUMAN BRAIN SODIUM DEPENDENT INORGANIC
; TITLE OF INVENTION: PHOSPHATE COTRANSPORTER AND RELATED NUCLEIC ACID COMPOUNDS
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: United States of America
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/647,481
; FILING DATE: 14-May-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/430,033
; FILING DATE: 27-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Gaylo, Paul J.
; REGISTRATION NUMBER: 36,808
; REFERENCE/DOCKET NUMBER: X-10006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 276-0756
; TELEFAX: (317) 276-3861
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 560 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-647-481-2

Query Match          33.1%; Score 940; DB 1; Length 560;
Best Local Similarity 39.5%; Pred. No. 1.6e-91;
Matches 193; Conservative 93; Mismatches 162; Indels 40; Gaps 8;

QY 53 DGEESTDRT---PLLP-----GAPRAEAPVCCSARVNLALIAFGFPIVALRVNLSVAL 105
DB 38 DGRPVTTQTRDPVVDCTCFGLPR-----RYIIAMSGIGFCISGIRCNLGVAI 87
QY 106 VDMVDSNTTLEDNRRTSKACEHSAPRIKYHNQTKKKQWDAETOGWILGSEFFYGYITQI 165
DB 88 VSMVNNSTT-----HRGHHVVVQKAQ---FSWDBETVGLIHGSFWMGYITQI 132
QY 166 PGGVVASKIGKMLGFGILGTAVLTFTPIADLGVGPLILVRLALEGLGEGVTFPAMHA 225
DB 133 PGGFICOKFANRVFGFAIVATSTLNLIPSAARVHGCIVFVRIILOGLVGEGVTPACHG 192
QY 226 MMSWAPPLERSKLLSTSYAGAOIGTVISLPGIICYYNMNTVVFYFFGTIGIFFWLW 285
DB 193 IWSKMAPPLERSRLATTAFCGSYAGAVVAMPPLAGVLVQYSGMSVFFVYVGSFGIFFWLW 252
QY 286 IWLVSDFPQHKRIASHKEYI-----LSLRNQLSQKSVPMVPIILKSLPLMAIVAH 339
DB 253 LTVSYESPALHPSISEERKTIEDDAIESAKLMP-LTKSTPMRRPFTSPVAILVAN 311
QY 340 FSYNMTFTYTLTLFTYMEILRENVQENGLSLPYLGSWLCMILSGQADNLRAKMF 399
DB 312 FCGSMFTYLLISQPDVFEFVGFSEIKVGLVSLPLHVMITIIYPIGGQIADFLRSRIM 371
QY 400 STLCAVRIRISLIGMIGAVFLVAAFGICDYSILAVALLTISTTLGCGSSGFSFINHDLIA 459
DB 372 STINVRKLMNCGGFGMEATILLVGVY-SHSKGAIVISFLVAVGFSGFAISGFVNHDIA 430
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QY 460 PSYAGILGTTNTEATIPGMVGPVIAKSLTPDNTVGEMQVTFYIAAINFGAIFETIFA 519
DB 431 PRYASILMGISNGVITSGMVCPIIVGAMTKHKTREMOYVFLIASLVHVGCVLFYGVFA 490
QY 520 KGEVQWMA 527
DB 491 SGEKQWMA 498

RESULT 14
US-08-430-033A-2
; Sequence 2, Application US/08430033A
; Patent No. 5686266
; GENERAL INFORMATION:
; APPLICANT: Ni, Binhui
; TITLE OF INVENTION: HUMAN BRAIN SODIUM DEPENDENT INORGANIC
; TITLE OF INVENTION: PHOSPHATE COTRANSPORTER AND RELATED NUCLEIC ACID COMPOUNDS
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: United States of America
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/430,033A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gaylo, Paul J.
; REGISTRATION NUMBER: 36,808
; REFERENCE/DOCKET NUMBER: X-10006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 276-0756
; TELEFAX: (317) 276-3861
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 560 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-430-033A-2

Query Match          33.1%; Score 940; DB 1; Length 560;
Best Local Similarity 39.5%; Pred. No. 1.6e-91;
Matches 193; Conservative 93; Mismatches 162; Indels 40; Gaps 8;

QY 53 DGEESTDRT---PLLP-----GAPRAEAPVCCSARVNLALIAFGFPIVALRVNLSVAL 105
DB 38 DGRPVTTQTRDPVVDCTCFGLPR-----RYIIAMSGIGFCISGIRCNLGVAI 87
QY 106 VDMVDSNTTLEDNRRTSKACEHSAPRIKYHNQTKKKQWDAETOGWILGSEFFYGYITQI 165
DB 88 VSMVNNSTT-----HRGHHVVVQKAQ---FSWDBETVGLIHGSFWMGYITQI 132
QY 166 PGGVVASKIGKMLGFGILGTAVLTFTPIADLGVGPLILVRLALEGLGEGVTFPAMHA 225
DB 133 PGGFICOKFANRVFGFAIVATSTLNLIPSAARVHGCIVFVRIILOGLVGEGVTPACHG 192
QY 226 MMSWAPPLERSKLLSTSYAGAOIGTVISLPGIICYYNMNTVVFYFFGTIGIFFWLW 285
DB 193 IWSKMAPPLERSRLATTAFCGSYAGAVVAMPPLAGVLVQYSGMSVFFVYVGSFGIFFWLW 252
QY 286 IWLVSDFPQHKRIASHKEYI-----LSLRNQLSQKSVPMVPIILKSLPLMAIVAH 339
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Db 253 LTVSYESPALHPSISEERKYLIEDAIGESAKLMNPL-TKFTSPMRFFTSMPVAILIVAN 311
Qy 340 PSYNTFFYLLTLPTPYMKEILRFNVOENGLSSLPYLSWLCMILSGAADNLRAKMF 399
Db 312 FCRSMTFFYLLISQPDFFEEVFGFEISKVGLVSALPHLVMTIIVPIGGQIADFLRSRIM 371
Qy 400 STLCVRRIISLIGMIGPAVFLVAAGFGCDYSILAVALTISTTLGFCSSGFSINHLDA 459
Db 372 STTNVRKLMNCGFGMEATLLVVGY-SHSGVALISFLVAVGSGFAISGFVNHLDA 430
Qy 460 PSYAGILGTTNTFATIPGMVGVIAKSLTPDNTVGEMQTVFYIAAIVFGAIFFTLFA 519
Db 431 PRYASILMGISNGVGLSGVNCPIIVGAMTKHKTREEMQYVFLIASLVHGVIFYGVFA 490
Qy 520 KGEVONMA 527
Db 491 SGEKOPWA 498
RESULT 15
PCT-US96-05792-2
; Sequence 2, Application PC/TUS9605792
; GENERAL INFORMATION:
; APPLICANT: Paul, Binhui
; TITLE OF INVENTION: HUMAN BRAIN SODIUM DEPENDENT INORGANIC
; TITLE OF INVENTION: PHOSPHATE COTRANSPORTER
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: United States of America
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/05792
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/430,033
; FILING DATE: April 27, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Gaylo, Paul J.
; REGISTRATION NUMBER: 36,808
; REFERENCE/DOCKET NUMBER: X-10006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 276-0756
; TELEFAX: (317) 276-3861
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 560 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US96-05792-2
Query Match 33.1%; Score 940; DB 5; Length 560;
Best Local Similarity 39.5%; Pred. No. 1.6e-91;
Matches 193; Conservative 93; Mismatches 162; Indels 40; Gaps 8;
Qy 53 DGEESTDRT---PLLP-----GAPRAEAPVCCSARYNLAIAPFGFFIVYLRVNLISVAL 105
Db 38 DGRPVTTQTDRDPFVDDCTCGELPR-----RYIIAIVSGIGFCISFGIRCNLGVAI 87
Qy 106 VDWVDSNTLEDNRTSKACEHSAPRIKYHNQTKKYQWDAETQGMILGSEFFYGIITQI 165
Db 88 VSMVNNSTT-----HRGHHVVVQKXQ---FSWDEPVTGLIHGSEFFMGYIVTQI 132

Qy 166 PGGVYASKIGCKMLGFGILGTAVALTFTPIAADLGVPLIVLRALEGGEVTFPAMHA 225
Db 133 PGGFIOCKRAANRVFFFAIVASTLMMLIPSAARVYGCVIFRIIQLGVEGTYRACHG 192
Qy 226 MMSMAPPLERSKULISYAGAQLTVISLPLSGIICYYMMNTVYFFFGTIGIEMFLIM 285
Db 193 IMGKMAPPLERSRLATTACGSYAGAVVAMPPLAGVLVQSGMSVFYVVGSGFIEMVLFM 252
Qy 286 IWLVDTPQKHRIISHYEKEYT-----LSSLRNOLSSQSVVPWVPLILSLPMAIVAH 339
Db 253 LTVSYESPALHPSISEERKYLIEDAIGESAKLMNPL-TKFTSPMRFFTSMPVAILIVAN 311
Qy 340 PSYNTFFYLLTLPTPYMKEILRFNVOENGLSSLPYLSWLCMILSGAADNLRAKMF 399
Db 312 FCRSMTFFYLLISQPDFFEEVFGFEISKVGLVSALPHLVMTIIVPIGGQIADFLRSRIM 371
Qy 400 STLCVRRIISLIGMIGPAVFLVAAGFGCDYSILAVALTISTTLGFCSSGFSINHLDA 459
Db 372 STTNVRKLMNCGFGMEATLLVVGY-SHSGVALISFLVAVGSGFAISGFVNHLDA 430
Qy 460 PSYAGILGTTNTFATIPGMVGVIAKSLTPDNTVGEMQTVFYIAAIVFGAIFFTLFA 519
Db 431 PRYASILMGISNGVGLSGVNCPIIVGAMTKHKTREEMQYVFLIASLVHGVIFYGVFA 490
Qy 520 KGEVONMA 527
Db 491 SGEKOPWA 498

Search completed: June 7, 2006, 05:44:37
Job time : 53 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 7, 2006, 05:38:01 ; Search time 42 Seconds
(without alignments)
1227.909 Million cell updates/sec

Title: US-10-823-506-8

Perfect score: 2836

Sequence: 1 MAGAMTPPPVQPARPGF.....LPAKGEVQNMALNDHGHHRH 536

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	987	34.8	493	2	G88553
2	967	34.1	472	2	S28286
3	936	33.0	560	2	I59302
4	822.5	29.0	465	2	A56410
5	809.5	28.5	465	2	S69915
6	808	28.5	563	2	T43650
7	808	28.5	576	2	H88548
8	801.5	28.3	467	2	A48916
9	797.5	28.1	573	2	T23589
10	786.5	27.7	465	2	I39473
11	767.5	27.1	544	2	T24633
12	747	26.3	512	2	H84698
13	629.5	22.2	501	2	B89135
14	562	19.8	413	2	T01534
15	531	18.7	437	2	T45634
16	530.5	18.7	466	2	S40767
17	492.5	17.4	561	2	D84800
18	486.5	17.2	568	2	S44742
19	476.5	16.8	592	2	T25419
20	460.5	16.2	516	2	T24729
21	452	15.9	530	2	T29418
22	445	15.7	380	2	T29248
23	444.5	15.3	543	2	T32496
24	432.5	15.2	499	2	T15201
25	431	15.2	506	2	T29968
26	419.5	14.8	493	2	T25357
27	392.5	13.8	478	2	T33942
28	389.5	13.7	445	2	T23590
29	388.5	13.7	462	2	T34365

30	386.5	13.6	473	2	T31717	hypothetical prote
31	380.5	13.4	425	2	A90055	hypothetical prote
32	372	13.1	420	2	S44900	ZK652.10 protein -
33	370.5	13.1	428	2	AD0675	membrane transport
34	362	12.8	485	2	T24115	hypothetical prote
35	360	12.7	455	1	H69752	probable glucarat
36	357.5	12.6	455	2	T34366	hypothetical prote
37	357	12.6	452	2	AE0861	probable glucarate
38	355.5	12.5	659	2	T33557	hypothetical prote
39	353	12.4	516	2	T27092	hypothetical prote
40	349	12.3	450	2	A65061	probable glucarate
41	349	12.3	450	2	C85930	probable transport
42	349	12.3	450	2	A91085	probable transport
43	339.5	12.0	445	1	D65171	hypothetical 48.8
44	336.5	11.9	493	2	T19383	hypothetical prote
45	334	11.8	487	2	T23776	hypothetical prote

ALIGNMENTS

RESULT 1

G88553
protein C38C10.2 [imported] - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C/Accession: G88553
R/Anonymous, The C. elegans Sequencing Consortium.
S/Science 282, 2012-2018, 1998
A/Title: Genome sequence of the nematode C. elegans: a platform for investigating biolo
A/Reference number: A75000; MUID:9906613; PMID:9851916
A/Note: see websites genome.wustl.edu/genec/C_elegans/ and www.sanger.ac.uk/Projects/C_el
A/Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; an
A/Accession: G88553
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-493 <STO>
A/Cross-references: UNIPROT:Q03567; UNIPARC:UP1000013B804; GB:chr_III; PIDN:CAA79549.1;
C/Genetic8:
A/Genes: C38C10.2
A/Map position: 3

Query Match	Best Local Similarity	Score	DB 2: Length	DB 2: Gaps
Matches 194; Conservative 94; Mismatches 179; Indels 22; Gaps 6;				
QY	55	EESTRTPPLDGAAPRAAPVCCSARYNLAIAFFGFIVYALRVMLSVLVDMVDSNTT	114	
DB	2	EGATTKEPLV-----STREPALSLVNFGLVYMMRTNMSFAVVCVNNKNT	49	
QY	115	LEDNRKSKAPRHSAPIKVHHNOTGKKYQWDATQGNILGSPFYGYITTOIPGIVASKI	174	
DB	50	DTEGEKVRSGCKEWTPEVSNSSVIIG--BFDDDKQITGVNLSFFGYGSGQIIGHLASRY	108	
QY	175	GGKMLGFGIIGTAVLTLFPIAADGVGPLVIRALEGEGGVTPPAMAMSSNAPL	234	
DB	109	GGKRVVFTVLGSLTLPLNPAKRTSEYLAIRAIIGLQGTAPFAAMTMSWGPCPL	168	
QY	235	ERSKLSISYAGQAGTVISLPLSGIICYY---MMTVYVFYFGTIGIFWLLMIWLVD	291	
DB	169	ELSLVLTGVTAAGQIGNVILPLSGFLCEVGFQDGMGSIIFYIGVFGVLTAAVWVYSSD	228	
QY	292	TPQKHKRISYKEKEYLISLRNOLSSO---KSPVNPILKSLPMAIVVAHNSYNTFY	347	
DB	229	KPATHPRITPEEKQYIVTAVEASMGKDTGVPTPWKILITSPAVWACWAGHAGDGAY	288	
QY	348	TLTLPTTYKKEILRFVQNGEFLSLPYLGSWLCMILSQAADNLRAKNPFSTLCVRR	407	
DB	289	TMLVSLPSFLKQVLGLNLSLGAVALSPYATYALNAGVADTLRSKQIISTLNTERR	348	
QY	408	FSLIIGMIGPAVFLVAGFGICDYS-LAVAFLLTSTLGGFCSSGGSFINHLIDPASYAGIL	466	
DB	349	AMVALIIGQGIPLVAGVCGCGDVLVITFITCGMAISGQVAGFVVNYLEIAPFSGTV	408	

Db 47 RMOJALAHFGFAISFGIRSNFGVAKRMNNFT-----DAYGEVHE----- 88

Qy 140 KKYQWDAETGQWMLGSEFFGYITTOIGGYVASKIGGKMLGFGILGTAVLTLPPIAD 199

Db 89 KEFFWTGTGVGMWSSSEFFGYAASQIPAGVIAAPAPNKLPMILGILFASILNITATC- 146

Qy 200 LGVGP-----LIVRALGEGEVTFRAMHAMSSMAPPLERSKLLSISYAGOLGTIVIS 254

Db 147 LNFHFPDIDIFMVAIQWQGLALGVCYPRMGVMKYMAPPERSKLATTTTFGASGVWVG 206

Qy 255 LPLSGIICYYNMWTVYFFPGTIGIFWFLMIWLVSDTPQKHRIISHYEKEYI--LSSL 311

Db 207 LPASAVYVSHFSWSTPFFVFGALGIVWSILWIVSGSPETHGYISADKKYITREKGSV 266

Qy 312 RNOLSSQKSVPMVPIKSLPLMAIVAHFSYNMFYLLTLTPFYMEILRFNVOENGL 371

Db 267 AVKMTLTTLTPMRDMWSTAWMAIILCSFCRSMSPFLGLQNLTYMDVHLIDIKNSGLI 326

Qy 372 SSLPYLGSWLCMLISGQADNLRAKNFSTLCVRRISLIGMIGPAVFLVAAGFIC-- 428

Db 327 AIRPQGMCIYTLTSGQLSDYLRSSGKMTFAVKSYNTRG-----FTVEAVMLGCLAF 380

Qy 429 --DYSLAAVFLTISTVLGFCSSGFSINHLDIAPSYAGIILGINTPATIPGMVPIAK 486

Db 381 VRBPVIAVTFLLIACSGAGAVLSGFNVNHFIDAPRHAPIIMGIANGLAIAAG-VGGIYTN 439

Qy 487 SLTPDNTVGEWQTVFYIAAIVNFGAIFFTLFAKEVQWNA 527

Db 440 SLTYQNPDG-WKQVFLMAISIDIFGILFPLFAKGDVLPWA 479

RESULT 10

139473

Na+-dependent phosphate cotransporter - human

C/Species: Homo sapiens (man)

C/Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004

C/Accession: I39473

R: Miyamoto, K.; Tatemui, S.; Sonoda, T.; Yamamoto, H.; Minami, H.; Takeda, Biochem. J. 305, 81-85, 1995

A/Title: Cloning and functional expression of a Na(+)-dependent phosphate co-transporter

A/Reference number: I39473; MUID:95126933; PMID:7826357

A/Accession: I39473

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-465 <RES>

A/Cross-references: UNIPROT:Q14916; UNIPARC:UP1000016A56A; GB:ID28532; NID:9639841; PIDN:

Query Match 27.7%; Score 786.5; DB 2; Length 465;

Best Local Similarity 37.7%; Pred. No. 1.8e-54;

Matches 177; Conservative 79; Mismatches 186; Indels 27; Gaps 6;

Qy 74 PVCCSARYNLAIILAFGFFIVARVNLVALVMDVSNNT--LEDNRTSKACEHSAPI 131

Db 11 PGCFSEFYGLSFLVHCNCNVIITAOIMCLNLTVMVNVNSTDPHGJPNSTYKLLDNINPM 70

Qy 132 KYAHNQTGKKYQDAETGQWMLGSEFFGYITTOIGGYVASKIGGKMLGFGILGTAVLT 191

Db 71 -----YNSPDVQGIILSTSTYGVIIIOVPGYFSGIYSTKMGIFALCLSSVLS 120

Qy 192 LFTPIADLGVPLIVLRALEGEGVTPRAMHAMSSMAPPLERSKLLSISYAGOLGT 251

Db 121 LILPRAAGIVAVVCGRAVQGAAGIVATAQPEIYVKMAPPLERGLTSMSTISGFLGP 180

Qy 252 VISLPSGIICYYNMWTVYFFPGTIGIFWFLMIWLVSDTPQKHRIISHYEKEYIISL 311

Db 181 FYILVLTGVICBSLGMPMVFIYFGACCAVCLMFVLPYDDPKDHPICISGEKEYINSSL 240

Qy 312 RNOL-SSQKSVPMVPIKSLPLMAIVAHFSYNMTFTLLTLPTYKKEILRFVQENGF 370

Db 241 VQGVSSRSQSLPILKAILKISLPWAISIGSFTFFSHIMLYLPMFNSMLHVNIKENGF 300

Qy 371 LSSLPYLGSWLCMLISGQADNLRAKNFSTLCVRRISLIGMIGPAVFLVAAGFICDY 430

Db 301 LSSLPYLFAWICGNLAQSLDFELTRNLSVIAVRKLFTAAGFLPLPAIFGVLPLYSTP 360

Qy 431 SLAAVFLTISTTGFCSSGFSINHLDIAPSYAGIILGINTPATIPGMVPIAKSLT- 489

Db 361 YSIVIFLILAGANGSFCLGVPINGLDIAPRYEFT---KACSTLGMIGGLIASTLNG 416

Qy 490 -----PDNTVGEWQTVFYIAAIVNFGAIFFTLFAKEVQWNA 532

Db 417 LILKQDESA---WPKTFILMAAINVGLIFYLIVATRAELQDAKKEKH 462

RESULT 11

124633

hypothetical protein T07A5.3 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C/Accession: T24633

R: Buck, D.

A/Submitted to the EMBL Data Library, February 1995

A/Reference number: Z19915

A/Accession: T24633

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-544 <WIL>

A/Cross-references: UNIPROT:Q10046; UNIPARC:UP1000013C01E; EMBL:Z48055; PIDN:CAA88134.1

A/Experimental source: clone T07A5

A/Genetics:

A/Gene: CESP:T07A5.3

A/Map position: 3

A/Intons: 38/3; 87/3; 272/3; 322/3; 444/3; 476/3; 496/1; 517/2

Query Match 27.1%; Score 767.5; DB 2; Length 544;

Best Local Similarity 35.9%; Pred. No. 6.8e-53;

Matches 166; Conservative 89; Mismatches 164; Indels 43; Gaps 9;

Qy 80 RYNLAIILAFGFFIVARVNLVALVMDVSNNTLEDNRTSKACEHSAPIKYHNQTG 139

Db 47 RMOJALAHFGFAISFGIRSNFGVAKRMNNFT-----DAYGEVHE----- 88

Qy 140 KKYQWDAETGQWMLGSEFFGYITTOIGGYVASKIGGKMLGFGILGTAVLTLPPIA-- 197

Db 89 REFLMTGAEVGMWSSSEFFGYAASQIPAGVIAAPAPNKLPMILGILFASILNITATC- 146

Qy 198 ----ADLGVPLIVLRALEGEGVTPRAMHAMSSMAPPLERSKLLSISYAGOLGTVI 253

Db 149 FHPYTDIFV--WVQAVQGLALGVLPRAHGVKWFAPPLERSKLATTFATGSSGVMT 205

Qy 254 LPLSGIICYYNMWTVYFFPGTIGIFWFLMIWLVSDTPQKHRIISHYEKEYILSLRN 313

Db 206 GLPASAVYVSHFSWSTPFFVFGVGIIMSLIMYVSHSPETHGYISDDEKQVTEKID 265

Qy 314 ---QLSSQKSVPMVPIKSLPLMAIVAHFSYNMTFTLLTLPTYKKEILRFVQENGF 370

Db 266 VAVKNSISLTLTPMRDMWSTAWMAIILCTFCRSMGFLLGNOLTYMKDVLHIDIKNSGF 325

Qy 371 LSSLPYLGSWLCMLISGQADNLRAKNFSTLCVRRISLIGMIGPAVFLVAAGFIC-- 428

Db 326 ISIFPQGMCIYTLTSGQLCDYLRSSGKMTFAVKSYNTRG-----FTVEAVMLGCLAF 379

Qy 429 ---DYSLAAVFLTISTVLGFCSSGFSINHLDIAPSYAGIILGINTPATIPGMVPIA 485

Db 380 FVRDPVIAVTCVIACGSSGVLSGFNVNHFIDAPRHAPIIMGIANGLAIAAG-VGGMVT 438

Qy 486 KSLTPDNTVGEWQTVFYIAAIVNFGAIFFTLFAKEVQWNA 527

Db 439 NTVTYQNPDG-WKQVFLMAIDIFGVIFPLFAKGDVLPWA 479

RESULT 12

H84698

hypothetical protein At2g29650 [imported] - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004


```

QY 140 KKYOMDADTQOMIIGSFYGYITITQIPGVYASKIGGKMLGFGILGNATVLTFFPIAAD 199
Db 91 OGINSSATFVGIQSSFFWGYLTQILGGIMADKFGK----- 128
QY 200 LGVGLIVLRALLEGEGVTFPAMHAMWSSWAPLERSKLISYAGAQLGTVLISLPLSG 259
Db 129 -----GVAMPANNNMLSKMIPIVSEBRSRLATLVSGMYLSSVIGLANSF 171
QY 260 IICYYMMNTVYFFYFFGTGIGFWFLIMLVSDTPQKHKRISHYEKEYILLSSRLNQLSSQK 319
Db 172 MLITKFGMPSVYFSGSLGSIFLLMLKFAVSSPDDEDLSEEEKVILGSKXPR-EBVT 230
QY 320 SVPMWPIILKSLPLMAIVVAHESYNNTFYTLITLTPT-----MKEL 361
Db 231 VIPWLLISKRPVWMLIISHFCHNMGFTILITMPTTYNQABSSASVYISL.FNIFCEBV 290
QY 362 RFNVQENGFSLPLTGLSMLCMIILSGAADMLRAKMNSTLCVRIFSLIGMIGPAVLY 421
Db 291 KFNLTRESLLCLLP-----MLTN-----AVPAN 313
QY 422 AAGFTGCDYSLAVAFLTISTLLGFCSSGFSINHLDIAPSYAGIILGTTNTPATIPGVNG 481
Db 314 IGGWIA--DTLVSRSLITNGSDAFQSGGLSNHODIPRAYGVILGLSNTAGVLAGVGF 371
QY 482 FVIAKSLTLPDNTVGEMQTVFYIAAANVFGAIFLTFKGE 522
Db 372 TAATGYILQR--GSMDDVFKVAALVYLIGTLVWMLFATGE 409

```

RESULT 15
T45634

hypothetical protein F13112.30 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
 C:Accession: T42634
 R:Christine, N.; Robert, C.; Brottier, P.; Wincker, P.; Catcollico, L.; Artiguenave, F.; Sanger, E.
 submitted to the Protein Sequence Database, November 1999
 A:Reference number: 223010
 A:Accession: T42634
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-537 <CHO>
 A:Cross-references: Q9SD75; UNIPARC:UPI0000A2A98; EMBL:AL133292
 C:Experimental source: cultivar Columbia; BAC clone F13112
 C:Genetics:
 A:Map position: 3
 A:Introns: 35/2, 153/3, 229/2, 350/3, 399/3, 445/3, 457/1
 A:Note: F13112.30

Query Match	Score	DB 2	Length
18.7%	531	537	

Best Local Similarity 27.6%; Pred No. 3.5e-34;
Matches 151; Conservative 86; Mismatches 195;
Indels 116; Gaps 15;

33 ASTPAHVGMRS-----PVRLARN-----DGEESTDRPTLLPGAPR 69

b
20 SSSSLTGVIVSSFDWRIPFLPERDARRKLVLTGRVNSPKFTGNTSYD---LGGIPR 75

70 AEAAPVCCSARYN-----LALLAFGGFIVYALRVNL SVA 104

b 76 HRLRVSCSDARRPPEETAELTAQPNFSEFTSERVKVAMLA-LALATCNADRVMSVA 134

105 LVDMVDSNTTLEDNRTSKACREHSAPIKVHNQGTCKYQWDAETOGWILGSPFYGVIIITQ 164

```

b      135 IV-----PLSLRG-----WSKSEGIWQSSFLMGYLISP 164

```

165 IPGGYVASKIGGKMLGFIGLSTAVLTFTPIADLGVGPLIVLRALGEGGVTPAMH 224

b

165 IAGGTLVDRIYGGKVMAMGVALMSLATFTLPWADSSIMWILLARAWGVAEGVALLPCMN 224

225 AMSSWAPPLERSKLSIYAGAOLCTVISLPLSGIICYMNTVYFFFGTIGIFWELL 284

225 NMVARWFPPIERSRAVGIMAGFOLGNVGLMLSPI LMSGGI YGPFVIFGLSGFLMLLV 284

[illegible]

Search completed: June 7, 2006, 05:43:41
Job time : 44 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 7, 2006, 05:44:52 ; Search time 17 Seconds
(without alignments)
398.588 Million cell updates/sec

Title: US-10-823-506-8

Perfect score: 2836
Sequence: 1 MAGAMTPRPVOPARPGF.....LFAKGEYONALNDHGRH 536

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 64914 seqs, 12641781 residues

Total number of hits satisfying chosen parameters: 64914

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: Published Applications_AA_New:*
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3: /EMC_Celerra_SIDS3/prodata/1/pubppaa/US06_NEW_PUB pep:*
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8: /EMC_Celerra_SIDS3/prodata/1/pubppaa/US60_NEW_PUB pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	801.5	28.3	467	6 US-10-511-937-2961	Sequence 2961, Ap
2	572.5	20.2	429	6 US-10-953-349-14670	Sequence 14670, A
3	503.5	17.8	264	7 US-11-293-697-3281	Sequence 3281, Ap
4	465	16.4	332	6 US-10-953-349-14671	Sequence 14671, A
5	381.5	13.5	425	6 US-10-471-571A-3576	Sequence 3576, Ap
6	371	13.1	288	6 US-10-953-349-14672	Sequence 14672, A
7	223.5	7.9	452	6 US-10-471-571A-1940	Sequence 1940, Ap
8	157.5	5.6	465	6 US-10-471-571A-2552	Sequence 2552, Ap
9	152.5	5.4	388	6 US-10-471-571A-3466	Sequence 3466, Ap
10	151	5.3	466	6 US-10-471-571A-5276	Sequence 5276, Ap
11	143	5.0	462	6 US-10-471-571A-4604	Sequence 4604, Ap
12	142.5	5.0	633	6 US-10-471-571A-4394	Sequence 4394, Ap
13	139.5	4.9	418	6 US-10-471-571A-2776	Sequence 2776, Ap
14	135	4.8	402	6 US-10-471-571A-5294	Sequence 5294, Ap
15	135	4.8	470	6 US-10-471-571A-3330	Sequence 3330, Ap
16	129	4.5	406	6 US-10-471-571A-3932	Sequence 3932, Ap
17	126.5	4.5	211	6 US-10-953-349-37919	Sequence 37919, A
18	125.5	4.4	353	6 US-10-471-571A-854	Sequence 854, App
19	125.5	4.4	447	6 US-10-471-571A-5314	Sequence 5314, Ap
20	121.5	4.3	461	6 US-10-471-571A-2426	Sequence 2426, Ap
21	121	4.3	403	6 US-10-471-571A-2714	Sequence 2714, Ap
22	120	4.2	400	6 US-10-471-571A-3540	Sequence 3540, Ap
23	119	4.2	551	7 US-11-318-813-7	Sequence 7, App11
24	117.5	4.1	195	6 US-10-953-349-37920	Sequence 37920, A
25	117.5	4.1	397	6 US-10-471-571A-5132	Sequence 5132, Ap

26	117	4.1	485	6 US-10-471-571A-4490	Sequence 4490, Ap
27	117	4.1	487	6 US-10-953-349-10426	Sequence 10426, A
28	117	4.1	493	6 US-10-953-349-10425	Sequence 10425, A
29	117	4.1	509	6 US-10-953-349-10424	Sequence 10424, A
30	117	4.1	551	7 US-11-318-813-2	Sequence 2, App11
31	117	4.1	551	7 US-11-318-813-38	Sequence 38, App11
32	113	4.0	326	6 US-10-953-349-33607	Sequence 33607, A
33	113	4.0	362	6 US-10-953-349-33606	Sequence 33606, A
34	113	4.0	370	6 US-10-953-349-33605	Sequence 33605, A
35	112.5	4.0	416	6 US-10-953-349-37181	Sequence 37181, A
36	112.5	4.0	443	6 US-10-953-349-37180	Sequence 37180, A
37	111	3.9	465	6 US-10-471-571A-5194	Sequence 5194, Ap
38	110.5	3.9	424	6 US-10-953-349-11588	Sequence 11588, A
39	110.5	3.9	460	6 US-10-953-349-11587	Sequence 11587, A
40	110.5	3.9	486	6 US-10-953-349-11586	Sequence 11586, A
41	107.5	3.8	366	6 US-10-471-571A-4838	Sequence 4838, Ap
42	107.5	3.8	727	6 US-10-471-571A-3846	Sequence 3846, Ap
43	107	3.8	387	6 US-10-471-571A-3580	Sequence 3580, Ap
44	105.5	3.7	192	6 US-10-953-349-37921	Sequence 37921, A
45	105.5	3.7	411	6 US-10-953-349-2483	Sequence 2483, Ap

ALIGNMENTS

RESULT 1
US-10-511-937-2961
Sequence 2961, Application US/10511937
Publication No. US20060088836A1
GENERAL INFORMATION:
APPLICANT: EXPRESSION DIAGNOSTICS, INC.
APPLICANT: Wohlgemuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc
APPLICANT: Prentice, James
APPLICANT: Morris, Macdonald
APPLICANT: Rosenberg, Steven
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
FILE REFERENCE: 50661200104
CURRENT APPLICATION NUMBER: US/10/511.937
CURRENT FILING DATE: 2004-10-19
PRIOR APPLICATION NUMBER: PCT/US2003/012946
PRIOR FILING DATE: 2003-04-24
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: US 10/325,899
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 3117
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2961
LENGTH: 467
TYPE: PRT
ORGANISM: Homo sapiens
US-10-511-937-2961

Query Match 28.3% Score 801.5; DB 6; Length 467;

Best Local Similarity 38.2% Pred. No. 2,4e-58;

Matches 179; Conservative 78; Mismatches 185; Indels 27; Gaps 6;

QY	74	PVCSARVNTALIAFFGFIVYALRVNLISVALVDMVDSNTT--LEDNRSTKACPEHAPI 131
DB	13	PGFCSFRYIGSFVHCNCNVITIKORACINLTITVYVNVNSTDPKPLPNTSTKLLDNINPM 72
QY	132	KVHNQTKYQWDAFTQGNILGSPFYGYITIQIPGVYASKIGKXLLGFGILGTVALT 191
DB	73	-----YXNSPDIGIILSTSYGVIIIQVPCVFGIYSTKMGICFALCLSSVL 122
QY	192	LFTPIADLVGSLIVLRALIEGEGVTTPAMAMMSNAPPIERKSLISTVAGAOJCT 251
DB	123	LILPPAGIGVAVVVCRAVOGAAGIVATQFEIYKAMPLEGRGLTSMSTSGFLLGP 182

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QY      VISLPSGICGYMMNTVYFYFEGGTGIFMFLIMLVSDTQKRIHSHYEKYEITSSL 311
QY      252  : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      FIVLVLTGVCISLGMPMVFIYFGACGACVCLLMPFLFDDPRKDHCICISSEKYEITSSL 242
QY      312  RNQT-SQSKSVBPVILKSLPLMAIVAHFSYNNMTFYTLTLTPLYMKEIILRNVOENG 370
Db      243  VOQVSSSSQSLPIKAILKSLPVMASIGSEFFFSNNHNTLTYPMFINMLHNINENG 302
QY      371  LSLSPYLSWLCMIISGQADNLRAKMNSTSCVRHIFSLIGMIGAVEFLVAAGFICQY 430
Db      303  LSSLPLPLRMICGNLAGQSDFFLTRNIIISVAVRCLFPAAGLPLAIFGVCPLYSSTP 362
QY      431  SLAAVFLTISTTLGGFCSSGSFINHLDIAPSIAGIILGTTNFATIPGAVGPYIANSLT- 489
Db      363  YSIVFLILAGATGFCIGGVFINGCIDIAPRYFGFI----KACSTLTGMIGGIASLTG 418
QY      490  -----PONTVGEMQTVFYIAAIVNFGAIFPLFKGEVONALMDHH 532
Db      419  LILKDDPESA---WERTFILMAIINTGLIFLYIVATAEIQPAKCKQH 464

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Db      63 RGPQSVFLAALAGASWLLMFXYATDPKSTASGVGESVLPVNKKIDTHNKK----- 114
      314 QLSQSKSVPMVPLIKSLPLMAIVAAHFSYNTFTLTLLPTYNKELLRNVQENGFLSS 373
      115 PLSAK--IPVKKILTSFPVMAIVNNFTFHALVLMNMTPTYPELGQLSLQDMGSSKM 172
      374 LPIYGLWLCMLISGOADNLRRAKNFSTLCVRRIFSILGIMGPAVFLVAGFICDYSLA 433
      173 MPYLMNLFPSNIGVADVILTRILISVTRKRLNVG-----FLVA-----SLA 218
      434 VAFVLTSTVLGG--FCSS-----GFSINHLDIAPSYAGILGINTPATIPGMV 480
      219 LVIIIPSRFTSGAVFCSSVALGFLALGRAGFAVNHMDIAPRYAGIWMGSVNSTAGTAGIV 278
      481 GPVI-----AKSLTPDNVTGE--MOTVFYIAAIAINFGAIFFLPAKGE 522
      279 GVDLTGKLEBAKKAANSDLSSPESWRAVFSIPGFLCIFSSVFLLFSTGE 328

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RESULT 5

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US-10-471-571A-3576
; Sequence 3576, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026927NO
; CURRENT APPLICATION NUMBER: US/10/471.571A
; PRIOR FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: GB-0107661.1
; NUMBER OF SEQ ID NOS: 5642
; SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 3576
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(425)
; OTHER INFORMATION: hypothetical protein
US-10-471-571A-3576

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```

Query Match      13.5%; Score 381.5; DB 6; Length 425;
Best Local Similarity 26.0%; Pred. No. 4.8e-24;
Matches 108; Conservative 81; Mismatches 177; Indels 49; Gaps 10;

```

```

      78 SARYNLAIIAIFGFFIYVALRVNLVALVMDVDSNTTLEDNRKTSKACPEHSAPIKVAHQ 137
      7 NVKMMFALAAFFIGVIAVMDRANISYIAKQMD-----DLGMITK----- 45
      138 TGKKYQMDAETQCMILGSPF--YGYIITQIDPGYVASKIGKMLIGFISLITAVLTFTPI 196
      46 -----PQFGLASFFSLGAYALMQVPSGMLAEKFGKRMKITTIALVWMSAFTILGTM 95
      197 AADLGGPLIVLALBSLGEGVTFRAMHAMSSWAPRLERSKLISIVAGAOGTIVSLP 256
      96 IKNHGL--IYLVFPLRGVGAAPMPSNAVNSFSGSKNERGKASSALLAGSFGPVLAPI 153
      257 LSGIICYYMMTVVFFFGTIGIFWFLIMVLVSDTPQKHRIISHYEKEYILSLRNQLS 316
      154 VTIAIVNAFVMAQVFIYFGAVGILMAVLMIAKDLDEGRMVNVEAKRFIMENRDI VAT 213
      317 SQKSVPMVPLIKSLPLMAIVAAHFSYNTFTLTLLPTYNKELLRNVQENGFLSLPY 376
      214 EKSSPMNDFFKFSFPAIAIOYFVVQFIITLPIIMPLTEVFHNFKEMS--ISLPLW 272
      377 LGSWLCMLISGOADNLR--RAKNFSTLCVRRIFSILGIMGPAVFLVAGFICDYSL 432
      273 LMFPLILSGAISDRVLGGRSKF-----VARGVIAIAGFIYFAVSIIFAVRTG---NL 324
      433 AVAFLTISTTLGGF--CSSGFS--INHLDIAPSYAGILGINTPATIPGMVGPVIA 485

```

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Db      325 YVSIFWLSLGGIGIGISMWMAATDLGRNFSGTVSGMMNLMGNIGALISPLIA 379

```

RESULT 6

```

US-10-953-349-14672
; Sequence 14672, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nicholas et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953.349
; PRIOR FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 14672
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-14672

```

```

Query Match      13.1%; Score 371; DB 6; Length 288;
Best Local Similarity 32.2%; Pred. No. 2.2e-23;
Matches 100; Conservative 51; Mismatches 100; Indels 60; Gaps 11;

```

```

      244 YAGAGLCTVSLPLSGIICYYMMMTVYFFFGTIGIFWFLIMVLVSDTPQK----- 295
      2 YLGAALGMLL-LP---TLVFRGPQSVFLAALAGASWLLMFXYATDPKSTASGVGESV 57
      296 ---HKRISHEKEYIISLRNQLSOKSVPMVPLIKSLPLMAIVAAHFSYNTFTLTLL 352
      58 LPVNKKIDTHNKK-----PLSAK--IPVKKILTSFPVMAIVNNFTFHALVLMN 107
      353 LPTYMKELRPNVQENGFLSSLPYLSWLCMLISGOADNLRRAKNFSTLCVRRIFSILG 412
      108 LPTYFELGLQSLQDMGSSKMPYLMNLFPSNIGVADVILTRILISVTRKRLNVG 167
      413 MIGRAVFLVAGFICDYSIAVAFLTISTLGG--FCSS-----GFSINHLDIA 459
      168 -----FLVA-----SLALVIIPSRFTSGAVFCSSVALGFLALGRAGFAVNHMDI 213
      460 PSYAGILGINTPATIPGMVGPVI-----AKSLTPDNVTGE--MOTVFYIAAIAIN 511
      214 PRYAGIWMGSVNSTAGTAGIVGVDLTGKLEBAKKAANSDLSSPESWRAVFSIPGFLCIF 273
      512 AIFFTLPAKGE 522
      274 SPVFLFSTGE 284

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RESULT 7

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US-10-471-571A-1940
; Sequence 1940, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026927NO
; CURRENT APPLICATION NUMBER: US/10/471.571A
; PRIOR FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: GB-0107661.1
; NUMBER OF SEQ ID NOS: 5642
; SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 1940
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(452)

```

OTHER INFORMATION: glycerol-3-phosphate
US-10-471-571A-1940

Query Match 7.9%; Score 223.5; DB 6; Length 452;
Best Local Similarity 22.9%; Pred. No. 4.4e-11;
Matches 109; Conservative 75; Mismatches 191; Indels 101; Gaps 19;

QY 83 LAILAFGFPPIVVA---LRNLVALVDMVDSNTLLEDRKTSKACPEHSAPLKHHNQ 138
DB 25 LRLQVFLGIFIGAGYVLLRKNFSLAM-----PALQEGCFKA----- 62
QY 139 GKXQVDAETQGIISFFYGYIITQIPGVYASKIGKMLGFGILGTAVLTLP---FTP 195
DB 63 -----ELGPAALSAVSIAYGFSKPEKGTVDNRNARIFLVGLALTAIVLMLNGFVP 113
QY 196 IADLGVPLIVLRALEGEGVTFPAMHAMSSMAPPLERSKLLISYGAQLGTVISL 255
DB 114 FPTS-GIGIMFVLLFLNGMFGQGWMPSGRVLVHMFVSERGSKTALMNVANHVGGINA 172
QY 256 PLS-GI-ICYNMNTY-----VFYFPGTIGFWFLMWLVSDTPQKH--KRISHYK 304
DB 173 PIAAMGITTAFINFGYLGKFGEGFYYPALALIIAISYVLLRDPQSGGLPPIETIKX 232
QY 305 EYLS---SLRNQSSOKSVPMPIKSLPLMAIVAHFSYNMTFYTLTLPTYMKEL 361
DB 233 DRAFTSKTLELETLI-KEILFKYVLLNNKVMALAPANITFYVRIGVLDMAVYLSSEK 231
QY 362 RFNVQENG---FL---SSLPYLGSMILSGAADNLAKMNFSTLCVRIFSLIGMIG 415
DB 292 HFPLKASGMAYFYEWAGIP--GTLICGYISDKLFKGRGPAGFFFWLGVTVFLIYMLN 349
QY 416 PA-----VFLVAAGFIGDYSLAVAFITSTLGGFCSSGSINHLIAP--SYAGILL 467
DB 350 PPGNAMLDNVSLAIGFLIYGPVLI-----GLQALDVPKKAQGTAA 392
QY 468 GITNFATIPGMV-----GPVIAKSLTPNTVGEQTVYIAAINVFAGIFFTL 517
DB 393 GLTGLFGYLFGAVMANIVLGAIVDKF-----GMDVGFIILTAISVFAMLSFIL 440

RESULT 8
US-10-471-571A-2552

/ Sequence 2552, Application US/10471571A
/ Publication No. US20060115490A1
/ GENERAL INFORMATION:
/ APPLICANT: CHIRON SPA
/ TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
/ FILE REFERENCE: P026927MO
/ CURRENT FILING DATE: 2003-09-12
/ PRIOR APPLICATION NUMBER: GB-0107661.1
/ PRIOR FILING DATE: 2001-03-27
/ NUMBER OF SEQ ID NOS: 5642
/ SOFTWARE: SeqWin99, version 1.03
/ SEQ ID NO 2552
/ LENGTH: 465
/ TYPE: PRT
/ ORGANISM: Staphylococcus aureus
/ FEATURE:
/ NAME/KEY: MISC FEATURE
/ LOCATION: (1)..(465)
/ OTHER INFORMATION: hexose phosphate transport
US-10-471-571A-2552

Query Match 5.6%; Score 157.5; DB 6; Length 465;
Best Local Similarity 20.2%; Pred. No. 1.1e-05;
Matches 99; Conservative 81; Mismatches 178; Indels 133; Gaps 23;

QY 86 LAFPGFPIYVALRVNLVALVDMD--SNTTLENNRSTSKACPEHSAPLKHHNQTKYQ 143
DB 39 VVEFYVYAMVYLIRNNFPAQOFLKEIIGLSTLE----- 71
QY 144 WDEMTQWILGSPFYGYIITQIPGVYASKIGKMLGFGILGTAVLTLP--IAADLG- 201

DB 72 -----LGYIGLAFSTIYGLGKTLIGFYVDGRNTRKILSFLLISAITVLIMGFVLSYFGS 126
QY 202 -VGPLIVPALSGLEGVTFPAMHAMSSMAPPLERSKLLISYGAQLGTVISLPLSGI 260
DB 127 VNGLLIVLMLGNGVFSQVSGPASPSTISRMAERTKGRGLGFWNTSHNIGALIA---GGV 183
QY 261 ICYNMNTYVFYFPGTIGFWF-----LLMIWLVSDTPQKH--KRISHYKEYILS 309
DB 184 ALMGAN---VFPHGNVIGFIFFPSYALLIGATLFIQDDDBELQMNABEIEWEPV-- 238
QY 310 SLRNQSSOKSVPM---VPIKSLPLMAIVAH--FSY-----NMTFYTLTLPTYM 357
DB 239 -DKNIDSGQMTKWEIFKKYIILGNPVYIWLICVSNVFYIVRIGIDMA-----PLVY 289
QY 358 KEILRFNVQENGFLSLPY--LGSMLCMLSGAADNLAKMNFSTLCVRIFSLIGMIG 415
DB 290 SEHIFPS--KQDAVNITFYFEIGALVASLWGVSDLLG-----RRALVAIG--- 335
QY 416 PAVELVAAGFIGDYSLAVAFITSTLGGFCSSGSINHLIAPSYAGILLGIT----- 470
DB 336 -CMFWIT--FVLFYTNATSVMMVNISL-----PALGALLFGPQ--LLIGVSLTGRV 382
QY 471 --NTFATIPGMVGPV-----IAKSLTPDN-----TVGEQTVFYIAAIN 508
DB 383 PKVAISVANQMTGSAFYLFQDSMAKVGALAIADPTNGINIGFYTLGWTGVFVYVAL 442
QY 509 VEGALFPTLPA 519
DB 443 FLGMILLGIYA 453

RESULT 9

US-10-471-571A-3466
/ Sequence 3466, Application US/10471571A
/ Publication No. US20060115490A1
/ GENERAL INFORMATION:
/ APPLICANT: CHIRON SPA
/ TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
/ FILE REFERENCE: P026927MO
/ CURRENT FILING DATE: 2003-09-12
/ PRIOR APPLICATION NUMBER: GB-0107661.1
/ PRIOR FILING DATE: 2001-03-27
/ NUMBER OF SEQ ID NOS: 5642
/ SOFTWARE: SeqWin99, version 1.03
/ SEQ ID NO 3466
/ LENGTH: 388
/ TYPE: PRT
/ ORGANISM: Staphylococcus aureus
/ FEATURE:
/ NAME/KEY: MISC FEATURE
/ LOCATION: (1)..(388)
/ OTHER INFORMATION: quinolone resistance
US-10-471-571A-3466

Query Match 5.4%; Score 152.5; DB 6; Length 388;
Best Local Similarity 19.7%; Pred. No. 2.3e-05;
Matches 76; Conservative 75; Mismatches 158; Indels 77; Gaps 13;

QY 150 GWILGSPFYGYIITQIPGVYASKIGKMLGFGILGTAVLTLPPIADLGVGPLIVLR 209
DB 41 GLVVAAPALSSQMTISPFQGLADKLKGLKILICIGLIFSSEPMFVGNHFSV--LMLSR 98
QY 210 ALBGLGEGVTFPAMHAMSSMAPPLERSKLLISYGAQLGTVISLPLSGIICYNMNTY 269
DB 99 VIGGMSAGMVPQVTGLIADISPSHQAKNFGYMSAIIINSGLFGIGFMA--EVSIRM 157
QY 270 VVEFYFPGTIGFWFLMWLVSDTPQKHKRISHYKEYIISLRNQLSSOKSVPMVPIKLS 329
DB 158 PFPFAGALGILAFIATISVLTHD--PKKSTTSGFQ-----LEPQLITK--INMKVFITP 207
QY 330 LPLMAIVAHFSYNMTFYTLTL-LPTYMKELRFNVQENG-----FLS 372

Db 208 VILTLVLSFGLSAETIYSLYTADKVNYSPKDISIAITGCGIFGALFOIYFEDEKMKYFS 267
QY 373 SLPLVIG-----SWFCMLISGOADNLRAKNFSTLCVARIISLIGMGAFLVAAGRTG 427
Db 268 ELFTIAMSLSYSVVLLILVLPAND---YWSIMLSIF-VVITGDMRPAI----- 313
QY 428 CDVSLAAVFLTISTTLGFCSSGSINHLDIAPSVAGILGILITNTFATIPGMVGVIAKS 487
Db 314 -----TNYFS-----NLAGERQSGAGLNGSTFTSMGNFISGLIAGA 349
QY 488 LTPDNTVGEWQTVFYIAAIVFCAI 513
Db 350 LFDVHI-----EAPIYMAIGVSLAGV 371

RESULT 10
US-10-471-571A-5276
; Sequence 5276, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026927WO
; CURRENT APPLICATION NUMBER: US/10/471,571A
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: GB-0107661.1
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 5642
; SOFTWARE: SeqwIn99, version 1.03
; SEQ ID NO 5276
; LENGTH: 466
; TYPE: PR
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(466)
; OTHER INFORMATION: hypothetical protein
US-10-471-571A-5276

Query Match 5.3%; Score 151; DB 6; Length 466;
Best Local Similarity 22.0%; Pred. No. 3.8e-05;
Matches 93; Conservative 66; Mismatches 154; Indels 110; Gaps 17;

QY 153 LGSFPGYIITQIPGVYVASKIGKMLGFGILGTAV---LTLPPIADLGVGPLVL 209
Db 55 LSLPLFAGLFI--VGAGVADKFGKRVKITVGLINNVGSLIITPLPAFLITG----R 107
QY 210 ALBGLGEGVTFPAMHAMSSWAPPLERSKLSISVAGAOIGTVISLPLSGIICYNNMTY 269
Db 108 IIGGLSAAICIMPSTLAINNEYIGTRORALSYWSISGWSGSGICTLFGGLMATYIGMR 167
QY 270 VFYFPGTIGIFWFLMWLVSDTPQKH---KRISHYEKEYILSSL-----RNQLS 316
Db 168 IF-----VVSILTLTLMAYLIKHAPEYKAEPKIGKMAKAKKFDVGLVILVMTLSLVII 223
QY 317 SOKS-----VPMV-----PIKSLPLMAIIVAHFSYN 343
Db 224 TQTSHGVLVPLILGLIVFICSLVGFVYENKIKAPLVDPSIFKNNGYSGATISNPLN 283
QY 344 WFTYTLTLTLPTWKELIRFNVQENGFLSLPYLGSWLCMILSGOADNLRAKNFSTLC 403
Db 284 GVGAGLIVINTYYQOGLGNSSQGTGYI-SLTYILITVLSMIRVGEKI--LSQHKRPL 340
QY 404 VRIIFSLIGMI-----GPAVFLVAAGFICGDYSLAAVFLTISTTLGFCSSGSFSINHL 457
Db 341 LSGGFVYIGLILSLFLPLPEVWYIISIVG-----YLLFGTGLG-----LY 381
QY 458 IASVYAGILGINTFATIPGMVGVIAKSLTPDNTVGEWQTVFYIAAI-NVPG-AIFF 515
Db 382 ATPS-----TDT-----AVASAPDUSGVAAGVYKMASSLGNAGVAVSG 421
QY 516 TLF 518

Db 422 TVY 424

RESULT 11
US-10-471-571A-4604
; Sequence 4604, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026927WO
; CURRENT APPLICATION NUMBER: US/10/471,571A
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: GB-0107661.1
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 5642
; SOFTWARE: SeqwIn99, version 1.03
; SEQ ID NO 4604
; LENGTH: 462
; TYPE: PR
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(462)
; OTHER INFORMATION: hypothetical protein
US-10-471-571A-4604

Query Match 5.0%; Score 143; DB 6; Length 462;
Best Local Similarity 21.8%; Pred. No. 0.00017;
Matches 94; Conservative 65; Mismatches 173; Indels 100; Gaps 19;

QY 153 LGSFPGYIITQIPGVYVASKIGKMLGFG---ILGTAVTLTLPPIADLGVGPLVL 208
Db 53 LPLFSGMEV--VGAGLADKIGRVKMTNIGLISITGSA-LITTLVPAFLITG----- 104
QY 209 RALEGLGEGVTFPAMHAMSSWAPPLERSKLSISVAGAOIGTVISLPLSGIICYNNMT 268
Db 105 RVIGVSAACIMPSTLAINMKTYYOGAERQALSYWSISGWSGSGICTLFGGAVATTMGR 164
QY 269 VFYFPGTIGIFWFLMWLVSDTPQKHKRISHYEK----- 304
Db 165 WIFIF---SIIYAVLSMLIKIGPEYKSEITMTHKFDVAGLIVLVMTLSLVNVIYKGA 220
QY 305 -----EYILSLRNQLSQKSV--PMV--PIKSLPLMAIIVAHFSYNTFY 347
Db 221 ALGYTSLMFGGLAIVIAVAFIFPLANVEKKVDNPLIDFKLENNKYTGATTISNPLN-GFA 279
QY 348 TLTTLPTWKELIRFNVQENGFLSLPYLGSWLCMILSGOADNLRAKN-----FST 401
Db 280 GTLIVANTFVQOGLGYALQAGYL-SITYLIMVLMIRVG---EKLQKSGSRPMLGT 335
QY 402 LCYRRIIFSLIGMI-GPAVFLVAAGFICGDYSLAAVFLTISTTLGFCSSGSFSINHL 460
Db 336 FIWITGIALISLVFLPQIFVY---ISC---VWGYLCFGLGIVATPS-----TDTAI 382
QY 461 SYA-----GILLGITNTFATIPG-----MGEVIAKSLTPDNTVGEWQTVFYIAA 505
Db 383 SNAPLDKVGVAAGIYKMASSLGAFAVAGVAVATATSIHTGAMLMWNVL--M 439
QY 506 AINVFCAIFFTL 517
Db 440 GIMAFIALIFAI 451

RESULT 12
US-10-471-571A-4394
; Sequence 4394, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026927WO

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; CURRENT APPLICATION NUMBER: US/10/471.571A
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: GB-0107661.1
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 5642
; SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 4394
; LENGTH: 643
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(643)
; OTHER INFORMATION: hypothetical protein
US-10-471-571A-4394

Query Match
Best Local Similarity 5.0%; Score 142.5; DB 6; Length 643;
Matches 111; Conservative 72; Mismatches 186; Indels 171; Gaps 24;

QY 79 ARYNLAIAFFGFPIYVALRVNLSVALVDVNDSTTIEDNRTSKACEHSAPIRVHINOT 138
DB 137 SRGKIIAALIFGFIATLNTQTLNVALPKI--NT----- 168
QY 139 GKRYQMDAETQGMILGSEFY--GYITQIPGQYVASKIGKMLGFGILGTAVLTLPPI 196
DB 169 --EPNISASTGQHLMTGFMVLNGLIPIT--AYIFNKYSRKLPVALVLTFTIGSLCAI 224
QY 197 AADLGVPFLIVLRALEGLGEGVTFPPAMAMSSWAPLERSKLISISVAGAOGLTV--- 252
DB 225 SNNFPI--MMVGRVLQIAGAGVLMPLGSIYITITYPEKR-----GAMQTMGIAM 273
QY 253 -----ISLPSGIIICYMNTVYFPGTIGIF-----WELIMVLV--SPTP--- 293
DB 274 ILAPALGPTLSGYIVQNYHNMVMEFGMFTIGIILIGFVWFKLYQYTTNPKADIPGIIIF 333
QY 294 -----QKRRISHYEKE-----YILSLRNQLSQKSVWVPIKSLP 331
DB 334 STIGFGALVYGFSEAGNKGMSVEIETMFAIGIIFILFYIRELRMSPMLEVLKFPPT 393
QY 332 LMAIVAHFSYNTFYTLTLPTMYKEILRENVQENGLSSLPYLGSMICMLI---SQQ 388
DB 394 FTLTITINMVMVLISYGMILLPTYLQNLRGFSALDGLL-LLP--GSLIMGLGPPAGK 450
QY 389 AANNLRK-----WNFSTL-----CVRRIFSLIGICPAY----- 418
DB 451 LLDITIGLKPLAIFGIAMVTYATWELTYLNDPTPYMTIGIYVLSFGMAFTMMMTVAI 510
QY 419 -----FL-----VAAGFIGDYSILAVAFITSTT--LGFCSSGFSIN----- 454
DB 511 NALPGLASHGNAPLNTMRQLASIGF--AIIYVMTTQTTQHLSAFGBELDKTNPVVD 568
QY 455 HL-DIAPSYAG-----ILLGITNTFATIPGMVGPVIAKSLTPDNTVGEWQVFIYAAI 507
DB 569 HMBELASQYGEGGAKMKVLLQFVVKLATVEGINDAFIV-----ATIPSIIALI 616

RESULT 13
US-10-471-571A-2776
; Sequence 2776, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026927WO
; CURRENT APPLICATION NUMBER: US/10/471.571A
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: GB-0107661.1
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 5642
; SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 2776
; LENGTH: 418

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; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(418)
; OTHER INFORMATION: hypothetical protein
US-10-471-571A-2776

Query Match
Best Local Similarity 4.9%; Score 139.5; DB 6; Length 418;
Matches 78; Conservative 70; Mismatches 169; Indels 65; Gaps 16;

QY 168 GYVASKIGKMLGFGILGTAVLTLP-----TPAADLGVPFLIVLRALEGLGEGVTFPA 222
DB 70 GKLGDIISRKMMVLRALLGLAVCLFMAICTTPTL-----QVLVRLQLGFGVAV-DA 121
QY 223 MHAMSSWAPLERSKLISVAGAOGLTVISLPLSGIICYMNTVYFPGTIGIIFNF 282
DB 122 SSAPASAEAPAEEDRGVILGRLOSVSAGSLVGLGIVASIIIGFSAIIM--SIIVTF 178
QY 283 LLMIV-----LVSDTPQKRRISHYEKEYILSLRNQLSQKSVWVPIKSLPLMAIYVA 338
DB 179 IVCIFGALKIETTHMPKSGTQTPVINKG--IRRSFQCLCTQTC-----RFIIV 225
QY 339 HFSYNTFYTLTLPTMYKEILRENVQEN--GFLSSLPYLGSMICMLISGQADN--L 393
DB 226 GVLANFAMQGMILFALSPASSVNHRTAIDRSVIGFLQSAFWTASIIAPLMGRFNDKSYV 285
QY 394 RAKMNSTLCVRKIFSLIGICGAVFLVAAGF--GCDYSL--AVAFITISTLGFCSS 449
DB 286 KSVYIATATJACGSALIGLATNIEFLMAARILOGLTYALIQSVNFVVA-----CHQ 340
QY 450 GFGINHLDIAPSYAGILGINTTFATIPGMVGPVIAKSLTPDNTVGEWQVFIYAAIYV 509
DB 341 -----QAKGFVGGTNSMLYVGOILGSLGAITSYTPA---TTFIVMGVFA 386
QY 510 FGAIFFTLPAKGEVQNMALNDH 531
DB 387 VSSLFLIC--STITN-QINDH 404

RESULT 14
US-10-471-571A-5294
; Sequence 5294, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026927WO
; CURRENT APPLICATION NUMBER: US/10/471.571A
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: GB-0107661.1
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 5642
; SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 5294
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(402)
; OTHER INFORMATION: hypothetical protein
US-10-471-571A-5294

Query Match
Best Local Similarity 4.8%; Score 135; DB 6; Length 402;
Matches 92; Conservative 77; Mismatches 182; Indels 120; Gaps 20;

QY 81 YNLALIAFFGFPIYVALRVNLSVALVDVNDSTTIEDNRTSKACEHSAPIRVH 134
DB 6 FKLSIMKLPFTFI-----LSIFIVGMVMMVAGIMNLSQDLHSEA----- 46

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Qy 135 HNQTKKYQMDAETQGMILGSFYYGIITQIPGGVASKIGKM-----LLGFGIL 185
Db 47 -----VGGVLNMYKALTFPAICGPIVLKLTNRSSRPVLLMTILIF-II 88
Qy 186 GTAVLTLPPIADLGVGPIVLRLPBLEGEGVTFFPAMHAWSSWAPPLERSKLLISYA 245
Db 89 GNGIIA----VAPNFSI--LVVGRHIISSAAALIIYKVALITAMLSAPKNGKMGIVYT 142
Qy 246 GAQGTYSILPLSGIICYYMMTYVFYFPGTIGIF-WFLMIMLVSDP-----PQKHRI 299
Db 143 GFSGANFVGPIGVITGDLVGMRYTFPLIIVSIIIVGLMMIYLPKQEIORGPNMHTP 202
Qy 300 SHYEKEYILSLRQLSQKSVPMWPIKSLPLMAIIVAFSYMTFFYTLTLPTWYKE 359
Db 203 SH-----EHHVTSKIIRP-AEVAKYLIITFVLIAHSYFVFINPLILNGHMS 251
Qy 360 ILRFNVQENGFLSLPYLGSWLCMLISGQAADNLRAK-WNESTLCVRIRFSLI-GMIGPA 417
Db 252 FVSLALVNG-----IAGVIGTSLGIGFSDKITSKMLMISVIFVMMMLNMLIPG 304
Qy 418 VFLLVAGPIGCDYSLAVAFLITSTLGGFCSSGFSINHLD-----IAPSYAGILL 467
Db 305 SGLLALGF-----IWNIMQWSTNPVQSGV-IQHVEGDTSQVMSWNNSLNAGIGV 355
Qy 468 GITVTFATIPGMVGPVIAKSLTPDNTVGEMQTFVYIAAIVFGAI-FTTL 517
Db 356 G-----GIIGGLVMTNHSV-----QAITTSAILGALGIIVFTL 390

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RESULT 15
US-10-471-571A-3330
; Sequence 3330, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026927WO
; CURRENT APPLICATION NUMBER: US/10/471,571A
; PRIOR FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: GB-0107661.1
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 5642
; SOFTWARE: Seqwln99, version 1.03
; SEQ ID NO 3330
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)-(470)
; OTHER INFORMATION: proline/betaine transporter
US-10-471-571A-3330

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Query Match          4.8%; Score 135; DB 6; Length 470;
Best Local Similarity 21.3%; Pred. No. 0.00079;
Matches 93; Conservative 74; Mismatches 172; Indels 98; Gaps 21;

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Qy 139 GKXKQW-----DAETQGMILGSF-----YGIITQIPG---GYVAS 172
Db 30 GNMMEWDFGVYATYATYIGANFSPVENADIRQMLTPAALAIAPLLRPIGGVFGIIGD 89
Qy 173 KIGGKMLGFGIGTAVLTLPPIADLGV-GPIVL--RALEGIGEGVFPAMHAM 226
Db 90 KYGRKVVLTSTIIIMAFSTLTIGLPSYDQIGLWAPILLARVLQGFSTGGEYAGANTY 149
Qy 227 WSSWAPPLERSKLLISYVAGNQLGTVISLPLSGIICYYMMTYVFYF-----FG--- 275
Db 150 VAESSPDKRNSLGS-----GLEIGT-----LSGYIASIMAVLTFPLTDEQMASFGWRI 200
Qy 276 --TIGIFWFLIMWL---VSDTPQKHRIKISHYEKEYILSLRNQSSQ---KSVPMWPIIL 327
Db 201 PFLIGLFLGLFGLYLRKRKLESP-----VENDVATQPERDININFLQII 244

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Qy 328 KSL--PLMAIIVAFSYNMTFFYTLTLTPYMKELIFNVQENGFLSLPYLGSWLCMIL 385
Db 245 RPYKDI FVCFVANVFENVTNNMTATLPYTLIEGVILKDATTTSSVLITCWMAIMIPLAM 304
Qy 386 SGQAADNLRAKWNESTLCVRIRFSLIGMIGPAVFLVAGFIGCDYSLAVAFLITSTLGG 445
Db 305 FGKLADRIKER-----KVF-LIGTGGLTFSSIIAFMLHLSQSFVV--IVIGIFILG 352
Qy 446 FCSGFSFINHLDIAPS--YAGI---LIGIT-NTEPATIPGMVGPVIAKSLTPDNTVGEMQT 499
Db 353 FFLSTYEATMPGSLPMTFYSHIRYRTLSVFNISVSIFGGTTPLVAVTLV--TKTGDPILA 410
Qy 500 VFYIAAIVNFGAIFFT 516
Db 411 PAYLTAISVIGFLVIT 427

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Search completed: June 7, 2006, 05:48:14
Job time : 18 secs

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Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 7, 2006, 05:34:31 ; Search time 301 Seconds
(without alignments)
1647.204 Million cell updates/sec

Title: US-10-823-506-8
Perfect score: 2836
Sequence: 1 MAGAMTPRPVQPARPGGF.....LFAKGEYQNALNDHGHHRH 536

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : UnlProt_7.2:*
1: unlprot_sprot:*
2: unlprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2621	92.4	495	1 S17A5_HUMAN	Q9NRA7 homo sapien
2	2621	92.4	495	2 O5S276_HUMAN	Q5S276 homo sapien
3	2329	82.1	495	1 S17A5_SHEEP	Q9MZD1 ovis aries
4	2298	81.0	495	1 S17A5_MOUSE	Q9BNR2 mus musculu
5	2298	81.0	495	2 O3TE25_MOUSE	Q9TE25 mus musculu
6	2298	81.0	495	2 O5Q0U0_RAT	Q9Q0U0 rattus norv
7	2072.5	73.1	484	2 O5ZL94_CHICK	Q9ZL94 gallus gall
8	1582.5	55.8	490	2 O4SGF2_TETNG	Q4SGF2 tetradon n
9	1051	37.1	473	2 O7O580_ANOGA	Q7O580 anopheles g
10	996.5	35.1	559	2 O9V167_DROME	Q9V167 drosophila
11	992	35.0	502	2 O9VDM0_DROME	Q9VDM0 drosophila
12	991	34.9	469	2 O7O579_ANOGA	Q7O579 anopheles g
13	987	34.8	493	1 YLID2_CAEEL	O03567 caenorhabdi
14	970	34.2	582	2 O920B7_MOUSE	Q920B7 mus musculu
15	970	34.2	582	2 O9J112_RAT	Q9J112 rattus norv
16	966.5	34.1	584	2 O8A477_BRARE	Q8A477 brachydanio
17	965.5	34.0	582	2 O9P2U8_HUMAN	Q9P2U8 homo sapien
18	965	34.0	582	2 O8BLF7_MOUSE	Q8BLF7 mus musculu
19	960.5	33.9	397	2 O4SY72_TETNG	Q4SY72 tetradon n
20	957.5	33.8	584	2 O5M818_BRARE	Q5M818 brachydanio
21	956	33.7	504	2 O4SAP9_TETNG	Q4SAP9 tetradon n
22	955	33.7	589	2 O8NDX2_HUMAN	Q8NDX2 homo sapien
23	954.5	33.7	588	2 O7TSF2_RAT	Q7TSF2 rattus norv
24	954.5	33.7	588	2 O8K1Q1_RAT	Q8K1Q1 rattus norv
25	946.5	33.4	474	2 O2PJ91_CAEEL	Q2PJ91 caenorhabdi
26	946.5	33.4	479	2 O23514_CAEEL	Q23514 caenorhabdi
27	945	33.3	601	2 O8BFU8_MOUSE	Q8BFU8 mus musculu
28	944.5	33.3	587	2 O5M817_BRARE	Q5M817 brachydanio
29	941	33.2	560	2 O9P2U7_HUMAN	Q9P2U7 homo sapien
30	939.5	33.1	576	2 O6INC8_XENLA	Q6INC8 xenopus lae
31	939	33.1	474	2 O623G6_CAEER	Q623G6 caenorhabdi

32	938	33.1	573	2	O4S7G2_TETNG	Q4S7G2 tetradon n
33	936	33.0	560	2	O3TXX4_MOUSE	O3TXX4 mus musculu
34	936	33.0	560	2	O62634_RAT	O62634 rattus norv
35	932	32.9	560	2	O6PCD0_HUMAN	O6PCD0 homo sapien
36	928.5	32.7	529	1	P1CO_DROME	Q9V785 drosophila
37	927.5	32.7	479	2	O32LF0_BOVIN	O32LF0 bos taurus
38	917	32.3	483	1	P1CO_DROAN	O61369 drosophila
39	913.5	32.2	576	2	O71513_XENLA	O71513 xenopus lae
40	910.5	32.1	461	2	O7PV86_ANOGA	O7PV86 anopheles g
41	910.5	32.1	502	2	O61IR3_CAEER	O61IR3 caenorhabdi
42	906	31.9	478	2	O5SZAI_MOUSE	Q5SZAI mus musculu
43	894.5	31.5	472	2	O7Q367_ANOGA	O7Q367 anopheles g
44	889.5	31.4	508	2	O7O1S5_ANOGA	O7O1S5 anopheles g
45	876	30.9	497	2	O9Y2C5_HUMAN	O9Y2C5 homo sapien

ALIGNMENTS

RESULT 1	ID	S17A5_HUMAN	STANDARD	PRT	495 AA.
AC	Q5NRA7; Q8NRS5; Q9UGH0;				
DT	07-JUN-2004, integrated into UnlProtKB/Swiss-Prot.				
DT	07-JUN-2004, sequence version 2.				
DT	07-FEB-2006, entry version 27.				
DE	Sialin (Solute carrier family 17 member 5) (Sodium/sialic acid cotransporter) (AST) (Membrane glycoprotein HP59).				
GN	Name=SLC17A5;				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;				
OC	Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), FUNCTION, AND TISSUE SPECIFICITY.				
RX	PubMed=11751519;				
RA	Fu C., Bardhan S., Cetateanu N.D., Manil B.D., Wang Y., Yan H.-P., Shi E., Carter C., Venkov C., Yakes F.M., Page D.L., Lloyd R.S., Mernaght R.L., Hellerqvist C.G.;				
RT	"Identification of a novel membrane protein, HP59, with therapeutic potential as a target of tumor angiogenesis.";				
RL	Clin. Cancer Res. 7:4182-4194 (2001).				
RU	[2]				
RP	NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), FUNCTION, TISSUE SPECIFICITY, AND VARIANT SD CYS-39, AND VARIANTS ISSD 268-SER-ASN-272 DEL; ARG-183 AND ARG-334.				
RX	MEDLINE=20047778; PubMed=10581036; DOI=10.1038/70585;				
RA	Verheijen F.W., Verbeek E., Aulia N., Baerens C.E.M.T., Havelaar A.C., Voosge M., Peltonen L., Aulia P., Galjaard H., Van der Spek P.J., Mancini G.M.S.;				
RT	"A new gene, encoding an anion transporter, is mutated in sialic acid storage diseases.";				
RL	Nat. Genet. 23:462-465 (1999).				
RU	[3]				
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 2).				
RX	PubMed=14702039; DOI=10.1038/ng1285;				
RA	Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R., Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H., Sekine M., Oobayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S., Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahara K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura M., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M., Tanomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori S., Tanai H., Kimura M., Watanabe S., Hiroaka S., Chiba Y., Ishida S., Oono Y., Takiguchi S., Watanabe S., Yosida M., Horuta T., Kusanagi J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N., Miasaishino K., Yuki H., Oshima A., Sasaki N., Aotsuka S., Yoshioka Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,				

RA Moriya S., Momiyama H., Saito N., Takami S., Terasushima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakabe H.,
RA Hienigskir H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kamagai A., Itakura S., Fukusumi Y.,
RA Fujimoto Y., Komiyama M., Tashiro A., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hiraio M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togeishi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano Y., Satcho T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagaue T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isegaki T., Sugano S.,
RT "Complete sequencing and characterization of 21,243 full-length human
RT cDNAs.",
RL Nat. Genet. 36:40-45(2004).
RN [4]
RN NUCLEOTIDE SEQUENCE (LARGE SCALE MRNA) (ISOFORM 2).
RP TISSUE=Colon;
RC MEDLINE=22388557; PubMed=12477932; DOI=10.1073/pnas.222603899;
RX Straube R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkin R.F., Jordan H., Moore T., Max S.I., Wang Y., Heien F.,
RA Diachenko L., Marusina K., Farmer A.C., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millaly S.J.,
RA Boeck S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.V., Huiyk S.W.,
RA Villalón D.K., Muray D.M., Sodegryn E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield J.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Maira M.A.;
RT "Genexion and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RN VARIANTS SD CYS-39 AND GGU-136, AND VARIANTS ISSD 268-SER--ASN-272
RP DEL; ARG-183; ARG-334 AND VAL-371.
RX PubMed=10947946;
RA Aul'a N., Salomaecki P., Timonen R., Verheljen F., Mancini G.M.S.,
RA Maensson J.-E., Aul'a P., Peltonen L.;
RT "The spectrum of SLG17A5 gene mutations resulting in free stalic acid-
RL storage diseases indicates some genotype-phenotype correlation.";
RL Am. J. Hum. Genet. 67:832-840(2000).
RN [6]
RN VARIANT SD CYS-39.
RX MEDLINE=22678449; PubMed=12794687; DOI=10.1002/atm.g.a.10246;
RP Martin R.A., Slaugh R., Natowicz M., Pearlman K., Orvisky E.,
RA Kranevich D., Kleta R., Natowicz M., Gahl W.A.;
RT "Stalic acid storage disease of the Salla phenotype in American
RT monozygous twin female sibbs.";
RL Am. J. Med. Genet. A 120:23-27(2003).
CC -1- FUNCTION: Primary solute translocator for anionic substances;
CC particularly it is a free stalic acid transporter in the lysosomes
CC (Probable).
CC -1- SUBCELLULAR LOCATION: Lysosome; lysosomal membrane; multi-pase
CC membrane protein (Probable).
CC -1- ALTERNATIVE PRODUCTS;
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=G9NRA2-1; Sequence=D1splayed;
CC Name=2;
CC IsoId=G9NRA2-2; Sequence=VSP 010482, VSP 010483;
CC Note=No experimental confirmation available;
CC -1- TISSUE SPECIFICITY: Found in fetal lung and small intestine, and
CC at lower level in fetal skin and muscle. In the adult, detected in
CC placenta, kidney and pancreas. Abundant in the endothelial cells
CC of tumors from ovary, colon, breast and lung, but is not detected

	-	DISEASES:	Defects in SLC17A5 are the cause of Salta disease (SD) [MIM:604369]; also known as Finnish type staturia, a slalic acid neurodegenerative disorder characterized by hypotonia, cerebellar ataxia and mental retardation. They are caused by a defect in the metabolism of sallic acid which results in increased urinary excretion of unconjugated salic acid, specifically N-acetylnuraminic acid. Enlarged lysosomes are seen on electron microscopic studies. Clinical symptoms of SD present usually at age less than 1 year and progression is slow.
	-	DISEASE:	Defects in SLC17A5 are the cause of infantile slalic acid storage disorder (ISSD) [MIM:269920]; also known as N-acetylneuraminic acid storage disease (NSD). ISSD is a severe form of sallic acid storage disease. Affected newborns exhibit visceromegaly, coarse features and failure to thrive immediately after birth. These patients have a shortened life span, usually less than 2 years.
	-	SIMILARITY:	Belongs to the major facilitator superfamily.
			Sodium/anion cotransporter family.
			Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NonDerivative license
CC			-----
CC		EMBL,	AEP44577; AAPF7769.1; ALT_INIT_ mRNA.
DR		EMBL;	AJ387747; CAB62540.1; -; mRNA.
DR		EMBL;	AK075320; BACI1546.1; -; mRNA.
DR		EMBL;	BG020961; AAH20961.1; -; mRNA.
DR		Ensembl;	ENSG00000119899; Homo sapiens.
DR		HGNc;	HGNc:10933; SLC17A5.
DR		MIM;	269920; phenotype.
DR		MIM;	604322; gene.
DR		GOM;	GO:0005887; C:integral to plasma membrane; TAS.
DR		GO;	GO:0005765; C:lysosomal membrane; TAS.
DR		GO;	GO:0005624; C:membrane fraction; TAS.
DR		GO;	GO:0005403; F:hydrogen:sugar symporter activity; TAS.
DR		InterPro;	IPIRO07114; MFS.
DR		InterPro;	IPIRO11701; MFS_1.
PFam;		PFO7690;	MFS_1; 1.
PROSITE;		PS50850;	MFS_1.
KW		Alternative splicing;	Disease mutation; Lysosome; Membrane; Symport;
KV		Transmembrane;	Transport.
XN		CHAIN	1 495 /Staln.
FT		TRANSMEM	42 62 /FTId=PRO_000020947.
FT		TRANSMEM	110 130 Potential.
FT		TRANSMEM	137 157 Potential.
FT		TRANSMEM	159 179 Potential.
FT		TRANSMEM	201 221 Potential.
FT		TRANSMEM	228 248 Potential.
FT		TRANSMEM	280 300 Potential.
FT		TRANSMEM	329 349 Potential.
FT		TRANSMEM	366 386 Potential.
FT		TRANSMEM	392 412 Potential.
FT		TRANSMEM	424 444 Potential.
FT		TRANSMEM	458 478 Potential.
FT		VASPLIC	274 276 ISS -> AGV (in isoform 2).
FT		VARSPLIC	278 495 /FTId=VP_010482.
FT		VARIANT	39 Missing (In isoform 2).
FT		VARIANT	39 R -> C (in SD); frequent mutation in Finland).
FT		VARIANT	/FTId=VAR_018684.
FT		VARIANT	K-> E (in SD).
FT		VARIANT	/FTId=VAR_018685.
FT		VARIANT	H-> R (in ISSD).
FT		VARIANT	/FTId=VAR_018686.
FT		VARIANT	Missing (In ISSD).
FT		VARIANT	/FTId=VAR_018687.
FT		VARIANT	P-> R (in ISSD).
FT		VARIANT	334 334 /FTId=VAR_018688.

FT	VARIANT	371	371	G -> V (in ISSD) . /FTID=VAR_018689.
	Query Match		92.4%	Score 2621; DB 1; Length 495;
	Best Local Similarity		100.0%	Pred. No. 1.9e-190;
	Matches	495;	Conservative	0; Mismatches 0; Indels 0; Gaps 0
QY	42	MRSPPRDLARNGEESTDPTPLPGAPRAEAPVCCSAAVNLALTFPGFFIYALRVNL	101	
DB	1	MRSPPRDLARNGEESTDPTPLPGAPRAEAPVCCSAAVNLALTFPGFFIYALRVNL	60	
QY	102	SVALVDWDSNTTLEDNRTSKACPEBSAIPKYHNOTGKKYQWDAETQGIIGSPFYGYI	161	
DB	61	SVALVDWDSNTTLEDNRTSKACPEBSAIPKYHNOTGKKYQWDAETQGIIGSPFYGYI	120	
QY	162	ITQIPGGYVASKIGGKMLGFGILGTAVLTFTPLIADLGVPILVLRALBEGEGVTEP	221	
DB	121	ITQIPGGYVASKIGGKMLGFGILGTAVLTFTPLIADLGVPILVLRALBEGEGVTEP	180	
QY	222	AMHAMWSSAAPPLERSKSLISIVAGQIGTIVSLPSGIICYYMMNTYVFFPGTIGIFW	281	
DB	181	AMHAMWSSAAPPLERSKSLISIVAGQIGTIVSLPSGIICYYMMNTYVFFPGTIGIFW	240	
QY	282	FLTWIIVSDPTQKKRISHYEKEYLLSLRNOLSKQVPMWPLIKSLPIVAIVAHNS	341	
DB	241	FLTWIIVSDPTQKKRISHYEKEYLLSLRNOLSKQVPMWPLIKSLPIVAIVAHNS	300	
QY	342	YNNFTYVTLTLPTWKELLRFNVQENGSLSPYLGSMVLCMILSGQADNLRAKNFST	401	
DB	301	YNNFTYVTLTLPTWKELLRFNVQENGSLSPYLGSMVLCMILSGQADNLRAKNFST	360	
QY	402	LCVRRIFSLIGMIGPAVFLVAAAGFGCDYSLAVAFITITTLGGFCSSGFSINHLDIAPS	461	
DB	361	LCVRRIFSLIGMIGPAVFLVAAAGFGCDYSLAVAFITITTLGGFCSSGFSINHLDIAPS	420	
QY	462	YAGILIGTNTFATIPGMVGPVIAASLTEDNVGEGQTYFYIAAANNVGAIPTFLFARG	521	
DB	421	YAGILIGTNTFATIPGMVGPVIAASLTEDNVGEGQTYFYIAAANNVGAIPTFLFARG	480	
QY	522	EVQNWALNDHHGHRH	536	
DB	481	EVQNWALNDHHGHRH	495	
RESULT 2				
QSSZ76_HUMAN PRELIMINARY; PRT; 495 AA.				
AC	QSSZ76	10-MAY-2005, integrated into UniProtKB/TrEMBL.		
DT	10-MAY-2005, sequence version 1.			
DT	07-FEB-2006, entry version 9.			
DE	Solute carrier family 17 (anion)/sugar transporter, member 5.			
GN	Name=SLC17A5; ORNames=RP3-397H23.3-001;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;			
OC	Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RA	Chapman J.			
RN	Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.			
RA	[2]			
RP	NUCLEOTIDE SEQUENCE.			
RA	Kay M.			
RL	Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.			
CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms			
CC	Distributed under the Creative Commons Attribution-NoDerivs License			
CC	EMBL; AL131972; CA120417.1; -, Genomic DNA.			
DR	EMBL; AL131972; CA120417.1; JOINED; Genomic DNA.			
DR	EMBL; AL131972; CA115635.1; JOINED; Genomic DNA.			

Query Match	92.4%	Score 2621	DB 2	Length 495
Best Local Similarity	100.0%	Pred. No. 1.9e-190		
Matches 495	Conservative 0	Mismatches 0	Indels 0	Gaps 0
Qy	42	MRSVPRLANDGESDTRTPILPGARAEAPVCCSARVNLATLAFPGFIYVALRNL	101	
Db	1	MRSVRLDARDGESDTRTPILPGARAEAPVCCSARVNLATLAFPGFIYVALRNL	60	
Qy	102	SVALVDVWDSNTTLEDNRTSKACEPSHAPIKVHNQTKKYQMDAETQWILGSFFGYI	161	
Db	61	SVALVDVWDSNTTLEDNRTSKACEPSHAPIKVHNQTKKYQMDAETQWILGSFFGYI	120	
Qy	162	ITQIPGGYVASKIGKMLGFGILGTVATLFTPEIADLGVPLIVRALGEGVTFP	221	
Db	121	ITQIPGGYVASKIGKMLGFGILGTVATLFTPEIADLGVPLIVRALGEGVTFP	180	
Qy	222	AMAHMSSMAPPLERSKLISVYAGADLVYISLPISGIIICYNNMTYVVFPEFTIGFW	281	
Db	181	AMAHMSSMAPPLERSKLISVYAGADLVYISLPISGIIICYNNMTYVVFPEFTIGFW	240	
Qy	282	FLIMTIVSPTRPOGKHRSIHYEKYIILSLRNQSSOKSPWVPLILKSLPLMAIVAHFS	341	
Db	241	FLIMTIVSPTRPOGKHRSIHYEKYIILSLRNQSSOKSPWVPLILKSLPLMAIVAHFS	300	
Qy	342	YNNTFYTLTLTLPTMYKEILRFVNOENGLSLPEYLGSWLCMLISGQADNLRKMNFT	401	
Db	301	YNNTFYTLTLTLPTMYKEILRFVNOENGLSLPEYLGSWLCMLISGQADNLRKMNFT	360	
Qy	402	LCVRRIRISLIGMIGPAVFLVAAAGTICGDYSLANAFLLTISTLLGFCSSGGSINHLDIAPS	461	
Db	361	LCVRRIRISLIGMIGPAVFLVAAAGTICGDYSLANAFLLTISTLLGFCSSGGSINHLDIAPS	420	
Qy	462	YAGILGINTTPTATIPGMVGPVIAKSLTPONTGEMQTVYIAAINVFGAIFPTLFAKG	521	
Db	421	YAGILGINTTPTATIPGMVGPVIAKSLTPONTGEMQTVYIAAINVFGAIFPTLFAKG	480	
Qy	522	EVQNMALNDHGRH 536		
Db	481	EVQNMALNDHGRH 495		

RESULT 3

S17A5 SHEEP

ID S17A5 SHEEP STANDARD; PRT; 495 AA.

AC Q9WZDT_

DT 07-JUN-2004, integrated into UniProtKB/Swiss-Prot.

DT 01-OCT-2000, sequence version 1.

DT 07-FEB-2006, entry version 22.

DE Stalim (soluble carrier family 17 member 5) (Sodium/stilic acid

DE cotransporter) (Membrane glycoprotein Sp55).

GN Name=SLC17A5.

OS Ovis aries (Sheep).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;

OC Pecora; Bovidae; Caprinae; Ovis.

OX NCBI_TaxID=9940;

XP [1]

NP NCULEOTIDE SEQUENCE [MRNA], FUNCTION, AND TISSUE SPECIFICITY.

CC TISSUE=Lung;

PubMed=11751519:
Fu C., Bardhan S., Ceteanu N.D., Wamil B.D., Wang Y., Yan H.-P.,
Shi E., Carter C., Venkov C., Yakes F.M., Page D.L., Lloyd R.S.,
Merrighan R.L., Hellerqvist C.G.,
RT Identification of a novel membrane protein, HPS9, with therapeutic
potential as a target of tumor angiogenesis.",
RL Clin. Cancer Res. 7:4182-4194(2001).
CC -1- FUNCTION: Primary solute translocator for anionic substances;
particularly it is a free fatty acid transporter in the lysosomes
(probable). Receptor for CM101, a polysaccharide produced by group
B Streptococcus with antipathogenic properties.
CC B SUBCELLULAR LOCATION: Lysosome; lysosomal membrane; multi-pass
membrane protein (potential).
CC -1- TISSUE SPECIFICITY: Significantly expressed in lung endothelial
cells, and much less in liver.
CC -1- SIMILARITY: Belongs to the major facilitator superfamily.
CC Sodium/anion cotransporter family.

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CC EMBL: AF24578; AAF7770.1; -, mRNA.
DR InterPro: IPR007114; MFS.
DR InterPro: IPR011701; MFS_1.
DR Pfam: PF07690; MFS_1; 1.
DR PROSITE: PS0850; MFS: 1.
KW Lysosome; Membrane; Receptor; Symport; Transmembrane; Transport.
KW CHAIN 1 495
FT TRANSMEM 42 62 /FTid=PRO_0000220949.
FT TRANSMEM 110 130 Potential.
FT TRANSMEM 137 157 Potential.
FT TRANSMEM 159 179 Potential.
FT TRANSMEM 201 221 Potential.
FT TRANSMEM 228 248 Potential.
FT TRANSMEM 289 309 Potential.
FT TRANSMEM 329 349 Potential.
FT TRANSMEM 366 386 Potential.
FT TRANSMEM 392 412 Potential.
FT TRANSMEM 424 444 Potential.
FT TRANSMEM 458 478 Potential.
SQ SEQUENCE 495 AA; 54536 MW; 649D7CA59B28272 CRC64;
Query Match 82.1%; Score 2329; DB 1; Length 495;
Best Local Similarity 86.3%; Pred. NO. 2.9e-168;
Matches 427; Conservative 39; Mismatches 29; Indels 0; Gaps 0;
OY 42 MRSPPVDLANDEESTDRTPLPGAPRAEAPVCCSARVNLALAFEGFPIYALRVNL 101
Db 1 MRSPPVDLANDEESTDRTPLPGAPRAEAPVCCSARVNLALAFEGFPIYALRVNL 60
OY 102 SVALVMDVDSNTLLEDRKTSKACPEHSAPIKVAHNNQCKYQNDALQGMILSFFFGYI 161
Db 61 SVALVMDVDSNTLLEDRKTSKACPEHSAPIKVAHNNQCKYQNDALQGMILSFFFGYI 120
OY 162 ITQIPGGYVASKGKMLFGFGLGTAVLTFPPIADLGGVPLIVRALEGAGVTFP 221
Db 121 ITQIPGGYVASKGKMLFGFGLGTAVLTFPPIADLGGVPLIVRALEGAGVTFP 180
OY 222 AMHAMSSMAPLERSKLISVAGAGLGVISLPLSGIICYYNMWTVYVFFGTIGIFW 281
Db 181 AMHAMSSMAPLERSKLISVAGAGLGVISLPLSGIICYYNMWTVYVFFGTIGIFW 240
OY 282 FLIMLWVSDTPQGHKRIKSHYEKEYILSLRNQSSQKSPVWPPIILSLPLMAIVAHFS 341
Db 241 FLIMLWVSDTPQGHKRIKSHYEKEYILSLRNQSSQKSPVWPPIILSLPLMAIVAHFS 300
OY 342 YNNTFTYLLTLPLPYMEKILRFNVQNGPLSLPYLGSWICMILSGAADNLRAKNMFT 401
Db 301 YNNTFTYLLTLPLPYMEKILRFNVQNGPLSLPYLGSWICMILSGAADNLRAKNMFT 360
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RESULT 4
S17A5 MOUSE
ID S17A5 MOUSE STANDARD; PRT; 495 AA.
AC OBBN82;
DT 07-JUN-2004, integrated into UniProtKB/Swiss-Prot.
DT 07-JUN-2004, sequence version 2.
DE 07-FEB-2006, entry version 21.
DE Sialin (Solute carrier family 17 member 5) (Sodium/sialic acid
cotransporter).
GN Name=S1c17a5;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
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RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORMS 1 AND 3).
RC STRAIN=C57BL/6J; TISSUE=Eye, and Skin.
RX PubMed=16141072; DOI=10.1126/science.1112014.
RA Carninci P., Kasukawa T., Katayama S., Gough J., Fritch M.C., Maeda N.,
Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
Bajic V.B., Brenner S.E., Batilov S., Forrest A.R., Zavolan M.,
Davis M.J., Wilm M., Kim M., Ohta T., Alt J.E.,
Ambesi-Impombi A., Apweiler R., Aturaliya R.N., Bailey T.L.,
Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chaik A.M.,
Chiu K.P., Choudhary V., Christoffels A., Clutier D.R.,
Crome M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,
Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
Guerginich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
Hill D., Hummel A., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
Jaki M., Kanapin A., Katoh M., Kawasawa Y., Kello J., Kitamura H.,
Kikuchi Y., Kohashi K., Krishnan S.P., Kruger A., Kummerfeld S.K.,
Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
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Wahlstedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
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Iida J., Imamura K., Itoh M., Kato T., Kawasaki H., Kawagashira N.,
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Nishio T., Okada M., Pleasy C., Shibata K., Shikata T., Suzuki S.,
Tegami M., Waki K., Watanabe A., Okamura-Oho Y., Suzuki H., Kawai J.,
Hayashizaki Y.,
RT "The transcriptional landscape of the mammalian genome.",
RL Science 309:1559-1563(2005).
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 2).
RC TISSUE=Olfactory epithelium;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

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 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
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 RA Richards S., Wozley K.C., Hale S., Garcia A.M., Gay L.J., Halyk S.W.,
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 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
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 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buttefield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Schenker A., Schein J.B., Jones S.J.M., Maria M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 CC Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: Primary solute translocator for anionic substances;
 CC particularly it is a free sialic acid transporter in the lysosomes
 CC (probable).
 CC -1- SUBCELLULAR LOCATION: Lysosome; lysosomal membrane; multi-pass
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 CC -1- ALTERNATIVE PRODUCTS:
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 CC IsoId=Q8BN82-2; Sequence=VSP_010484;
 CC Note=No experimental confirmation available;
 CC Name=3;
 CC IsoId=Q8BN82-3; Sequence=VSP_010485, VSP_010486;
 CC Note=No experimental confirmation available;
 CC -1- SIMILARITY: Belongs to the major facilitator superfamily.
 CC Sodium/anion cotransporter family.
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 CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
 CC Distributed under the Creative Commons Attribution-NonDerivs License
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 CC EMBL; AK029102; BAC26298.1; -; mRNA.
 CC EMBL; AK087395; BAC39859.1; -; mRNA.
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 CC MGI; MGI:1924105; Slc17a5.
 CC GO; GO:0016023; C:cytoplasmic membrane-bound vesicle; IDA.
 CC GO; GO:0005886; C:plasma membrane; IDA.
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RA PubMed:16141073; DOI=10.1126/science.1112014;
RA Carninci P., Kasukawa T., Katayama S., Gough J., Fritch M.C., Maeda N.,
RA Oyama R., Ravasi T., Lenhard B., Wells R., Kodzius K., Shimokawa K.,
RA Bajic V.B., Bremner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA Davis M.J., Wilming L.G., Altman J., Allen J.E.,
RA Ambesi-Implombito A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA Banasi M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA Chiu K.P., Choudhary V., Christoffels A., Clutierbuck D.R.,
RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,
RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA Hill D., Hummel L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA Jakt M., Kanapin A., Katoh K., Kawasawa Y., Kelso J., Kentland H.,
RA Kitzano H., Kollas G., Krishnan S.P., Kruger A., Kumari S.K.,
RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA Mottegu-Taber S., Mulder N., Nakano N., Nakachi H., Ng P.,
RA Nilsen R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavoni G., Pesole G.,
RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA Schombach C., Sekiguchi K., Sempile C.A., Seno S., Sees L., Sheng Y.,
RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA Sperling S., Stupka E., Sugita K., Sultana R., Takenaka Y., Taki K.,
RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yeai K.,
RA Yamashiki H., Zabarovsky E., Zhai S., Zimmer A., Hide W., Bult C.,
RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA Wahlstedt C., Macleod J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawaguchi N.,
RA Kawashima T., Kojima M., Kondo S., Kono H., Nakano K., Nimomiya N.,
RA Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,
RA Tagami M., Waki K., Watanabe A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA Hayashizaki Y.,
RA "The transcriptional landscape of the mammalian genome.",
RA Science 309:1559-1563(2005).
RA [3]
RA NUCLEOTIDE SEQUENCE.
RA STRAIN=ND;
RA MEDLINE=20530913; PubMed=1107661; DOI=10.1101/gr.152600;
RA RIKEN Genome Exploration Research Group and Genome Science Group
RA (Genome Network Core Team) and the FANTOM Consortium;
RA "Antisense transcription in the mammalian transcriptome.",
RA Science 309:1564-1566(2005).
RA [4]
RA NUCLEOTIDE SEQUENCE.
RA STRAIN=ND;
RA MEDLINE=22354683; PubMed=1246685; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nakado I., Osato N., Saito R., Suzuki H., Yamana K.I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schombach C., Gojobori T.,
RA Balderelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Brat D., Brusic V., Chochia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Fraser K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawai H., Kawasawa Y., Kedziercki R.M., King B.L.,
RA Konegaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Meglert D.R., Maltas L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Petrea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.V., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume M., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,
RA Yasunishi A., Yoshino M., Waterson R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.,
RA "Analysis of the mouse transcriptome based on functional annotation of
RA 60,770 full-length cDNAs.",
RA Nature 420:563-573(2002).
RA [5]
RA NUCLEOTIDE SEQUENCE.
RA STRAIN=ND;
RA MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kociba H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Stupka E., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Holman M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombauts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schombach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohseki S.,
RA Hayashizaki Y.,
RA "Functional annotation of a full-length mouse cDNA collection.",
RA Nature 409:685-690(2001).
RA [6]
RA NUCLEOTIDE SEQUENCE.
RA STRAIN=ND;
RA MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
RA "Normalization and subtraction of cap-trapper-selected cDNAs to
RA prepare full-length cDNA libraries for rapid discovery of new genes.",
RA Genome Res. 10:1617-1630(2000).
RA [7]
RA NUCLEOTIDE SEQUENCE.
RA STRAIN=ND;
RA MEDLINE=20530913; PubMed=1107661; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama U., Nishi K., Kitsuunai T., Taahiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuda S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RA "RIKEN integrated sequence analysis (RISA) system-384-format
RA sequencing pipeline with 384 multicapillary sequencer.",
RA Genome Res. 10:1757-1771(2000).
RA [8]
RA NUCLEOTIDE SEQUENCE.
RA STRAIN=ND;
RA Arakawa T., Carninci P., Fukuda S., Hashizume M., Hayashida K.,
RA Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
RA Kawai J., Kojima M., Kono H., Murata M., Nakamura M., Nimomiya N.,
RA Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watanabe A.,
RA Muramatsu M., Hayashizaki Y.,
RA Submitted (Apr-2004) to the EMBL/GenBank/DBJ databases.
RA [9]
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Query Match 81.0%; Score 2298; DB 2; Length 495;
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QY 42 MRSPVRDLARNDEESTDRTPLLPGAPRAEAPVCCSARYNLAIAAFGFFIYALRVNL 101
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 RP PubMed=15516337; DOI=10.1074/jbc.M411295200;
 RX Wreden C.C., Wlitzla M., Reimer R.J.;
 RT "varied mechanisms underlie the free stalle Acid storage disorders.";
 RL J. Biol. Chem. 280:1408-1416(2005).
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FX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L.H., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan J., Moore T., Wax S.I., Wang J., Heien F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalhe D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Placenta;
 RG NIH MGC Project;
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
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DR EMBL: AY800277; AA973775.1; -; mRNA.
 DR EMBL: BC097482; AA97482.1; -; mRNA.
 DR Ensembl: ENSRN00000009330; Rattus norvegicus.
 DR GO: GO:0016021; C:integral to membrane; IEA.
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 DR GO: GO:0005351; F:sugar porter activity; IEA.
 DR GO: GO:0005215; F:transporter activity; IEA.
 DR GO: GO:0006810; P:transport; IEA.
 DR InterPro: IPR007114; MFS.
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 DR Pfam: PF07690; MFS_1; 1.
 DR PROSITE: PS50850; MFS; 1.
 KM Membrane; Sugar transport; Transmembrane; Transport.
 SQ SEQUENCE 495 AA; 54323 MW; AAB0A29BA5D42094 CRC64;

Query Match 81.0%; Score 2298; DB 2; Length 495;
 Best Local Similarity 86.8%; Pred. No. 6.5e-166;
 Matches 428; Conservative 29; Mismatches 36; Indels 0; Gaps 0;

QY 42 MRSPVRDLARNDEESTDRTPLLPGAPRAEAPVCCSARYNLAIAAFGFFIYALRVNL 101
 1 MRPLRLRPGAGNDEESSDSTPLPGARQTEAPVCCSARYNLAIAAFGFFIYALRVNL 60
 DB SVALVDMVDSNTLTLDNRSTKCAPEHSAPIKVHNHNGKKYQMDAETQGMILGSFFGYI 120
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 QY 342 YNNFTFTLLTLPTTKKEILRFNVQENGFLSLPYLGSWLCMLISGQADNLRKKNFST 401
 301 YNNFTFTLLTLPTTKKEILRFNVQENGFLSLPYLGSWLCMLISGQADNLRKKNFST 360

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QY 402 LCVRRIFSLIGMIGPAVFLVAAGFICGDSYLAVALFTISTTLGCGFCSSGFSINHLDIAPS 461
DB 361 ISRRIRFSLIGMIGPAVFLVAAGFICGDSYLAVALFTISTTLGCGFCSSGFSINHLDIAPS 420
QY 462 YAGILLGTTTFAITPGMVGPIAKSLTPDNTVGEMQTVFYIAAINVFGAIFFTLPAKG 521
DB 421 YAGILLGTTTFAITPGMIGPIIAKSLTPDNTIKEMQTVFCIAAINVFGAIFFTLPAKG 480
QY 522 EVQNMALNDHGH 534
DB 481 EVQNMALSDHGH 493

RESULT 7
OSL194_CHICK PRELIMINARY; PRT; 484 AA.
AC OSL194;
DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.
DT 23-NOV-2004, sequence version 1.
DT 21-FEB-2006, entry version 13.
DE Hypothetical protein.
GN ORFNames=RCJMB04_7b17;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CB; TISSUE=Bursa;
RA Caldwell R.B., Kierzek A.M., Arakawa H., Bezzubov Y., Zaim J.,
RA Fiedler P., Kuter S., Blagoderstki A., Kostovska D., Kocer M.,
RA Plachy J., Carinci P., Hayashizaki Y., Buerstedde J.M.,
RT "Full-length cDNAs from chicken Bursa lymphocytes to facilitate
RT gene function analysis."
RL Genome Biol. 6:R6-R6(2005).
CC -1- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein (By
CC similarity).
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NonDerivs License
CC -----
DB EMBL: AJ719840; CAG31499.1; -, mRNA.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0005215; F:membrane; IEA.
DR GO: GO:0006810; P:transport; IEA.
DR InterPro: IPR007114; MFS.
DR InterPro: IPR011701; MFS_1.
DR Pfam: PF07690; MFS_1; 1.
DR PROSITE: PS00850; MFS_1.
KW Hypothetical protein; Membrane; Transmembrane; Transport.
SQ SEQUENCE 484 AA; 53557 MW; E9BDE09FES2D502 CRC64;

Query Match 73.1%; Score 2072.5; DB 2; Length 484;
Best Local Similarity 79.5%; Pred. No. 8.6e-149;
Matches 383; Conservative 47; Mismatches 51; Indels 1; Gaps 1;

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QY 295 KHKRI SHYEKEYILSLRNQLSOKSVPMVPIKSLPLMAIVAHFSYMMTFYLLTLTP 354
DB 243 THKISIRIEREYILSSLKQSLSTOKSVPMRPILESPLMAIVAHFSYMMTFYLLTLTP 302
QY 355 TYWKEILRFNVQENGLSSLPYGSWLCMILSGAANDIRAKNFTLTCVRIRFSLIGMI 414
DB 303 TYWKEILRFPAQNGFSLALPYFGCWLCTILSGQIDHLREKQNFSTVCRCFCFTLIGMI 362
QY 415 GPAVFLVAGFTGCDYSLAVPLTISTTLGCGFCSSGFSINHLDIAPSYAGILLGINTPA 474
DB 363 GPAVFLVAGFTGCDYSLAVPLTISTTLGCGFCSSGFSINHLDIAPSYAGILLGINTPA 422
QY 475 TTPGMVPIAKSLTPDNTVGEMQTVFYIAAINVFGAIFFTLPAKEVQNMALNDHGH 534
DB 423 TTPGMVPIAKSLTPDNTVGEMQTVFYIAAINVFGAIFFTLPAKEVQNMALNDHGH 482
QY 535 RH 536
DB 483 RH 484

RESULT 8
Q4SGF2_TETNG PRELIMINARY; PRT; 490 AA.
AC Q4SGF2;
DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE Chromosome 17 SCAR14597, whole genome shotgun sequence. (Fragment).
GN ORFNames=GSTEN00018669001;
OS Tetradodon nigroviridis (Green puffer).
OC Tetradodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetradodon.
NCBI_TaxID=99883;
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RP NUCLEOTIDE SEQUENCE.
RX PubMed=15496914; DOI=10.1038/nature03025;
RA Jullion O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
RA Mauceli E., Bounneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicard S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segutene B.,
RA Desliva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castellio L., Poulin J., De Berardinis V.,
RA Biemont C., Skalli Z., Cottolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Broctier P., Coutanceau J.-P., Guzy J.,
RA Paria G., Lardier G., Chappe C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin M., Scarpetti C.,
RA Wincker P., Lander E.S., Weissbach J., Roest Crolius H.,
RT "Genome duplication in the teleost fish Tetradodon nigroviridis reveals
RT the early vertebrate proto-karyotype."
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC Genoscope, Whitehead Institute Centre for Genome Research;
RG Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NonDerivs License
CC -----
DB EMBL: CAE01014597; CAG00280.1; -, Genomic DNA.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0005215; F:transport; IEA.
DR GO: GO:0006810; P:transport; IEA.
DR InterPro: IPR007114; MFS.
DR Pfam: PF07690; MFS_1; 1.
DR PROSITE: PS00850; MFS_1.

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RA Suton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abiri J.F., Agbayani A., An H.-U., Andrews-Plamnoch C., Baldwin D.,
RA Ballew R.M., Basu A., Bakendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Bortova D., Botchan M.R., Butler H., Cadieu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrera S., Fleischmann W.,
RA Fessler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glaeser K.,
RA Glodok A., Gong F., Gottrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegawa C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasco P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskearn D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E.C., Spralling A.C., Stapleton M., Strong R., Sun E.,
RA Svitzkae R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Waasman D.A., Weinstein G.M., Weisenbach J.,
RA Williams S.M., Woodard T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zhang L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RT "The genome sequence of *Drosophila melanogaster*." ,
RT Science 287:2185-2195(2000).
[2]
RA NUCLEOTIDE SEQUENCE.
RA MEDLINE=22426065; PubMed=12537568;
RA Celisner S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Harkins R.A., Laverly T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svitzkae R., Taber P.E., Wan K., Stapleton M., Suton G.G., Venter C.,
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,
RT "Finishing a whole-genome shotgun: release 3 of the *Drosophila*
RT *melanogaster* euchromatic genome sequence." ,
RT Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
[3]
RA NUCLEOTIDE SEQUENCE.
RA MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svitzkae R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celisner S.E.,
RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
RT a genomic perspective." ,
RT Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
[4]
RA NUCLEOTIDE SEQUENCE.
RA MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby W.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitefield E.J., Bayraktaroglu L., Berman B.P.,
RA Betencourt R., Celisner S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.,
RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
RT systematic review." ,
RT Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
[5]
RA NUCLEOTIDE SEQUENCE.
RA Berkeley *Drosophila* Genome Project;
RA Celisner S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,

RA Hoskins R., Stapleton M., Pacleb J., Park S., Svitzkae R., Smith E.,
RA Yu C., Rubin G.,
RT "Drosophila melanogaster release 4 sequence." ,
RT Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
[6]
RA NUCLEOTIDE SEQUENCE.
RA Submitted (JAN-2006) to the EMBL/Genbank/DBJ databases.
RA FlyBase;
CC -1- INTERACTION:
CC 024180:Def1; NbExp=1; IntAct=EBI-88239; EBI-149832;
CC -1- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein (By
CC similarity).
CC -----
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NonDerivs License
CC -----
DR EMBL: A8003491; AAF48230.1; -; Genomic_DNA.
DR Inact; Q9VYG7; -;
DR FlyBase; FBgn0030452; CG4330.
DR GO; GO:000515; F:Protein binding; IPI.
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DR InterPro; IPR011701; MFS_1.
DR Pfam; PF07690; MFS_1; 1.
DR PROSITE; PS50850; MFS; 1.
KW Membrane; Transmembrane; Transport.
KW SEQUENCE 559 AA; 61745 MW; 8C48402881046C70 CRC64;

Query Match 35.1%; Score 996.5; DB 2; Length 559;
Best Local Similarity 39.8%; Pred. No. 5,7e-67;

Matches 208; Conservative 91; Mismatches 171; Indels 53; Gaps 10;

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103 VALVDND-----SNTLEDNRTSCAPEHSAPIVHHN-----QTGKTYOMAEFG 150
91 VALVAVNQTALPHSNSVIDTDT--CP-LPAP--HHNGSDPNPQKEGFVMEATOG 143
151 WLGSFFGYIITQIRGGVVASKIGKMLGFIIGTAVLTFTPIAADLGVPILVRA 210
144 LVIGSFFGYVLTQVGGMAELVGGKTIYGVLTITAVFTLITPLAAHMDLPLVLVI 203
211 LBGIGGVTFPAMHAAMSWAPPLERSKLLSISYAGOLGTVISLPLSGITC---YVMW 267
204 LBSMGCVTYPPAMHALLAMIPLEBNKFAALVYVNSNGITVISMLACMLGSLPLGCV 263
268 TVVFYFFGTIGFVFLMTLVSDTPQKRIISHVEKEYILSLRNQ----- 314
264 PSAFYIFGLIGLIMFAMMYLVYDKPSDHPRISESEYIERSLOVORLINDLEABEE 323
315 -----LSQKSPVWPVILKSLPLMAIVVAHFSYNNFTYTLTLPTMKELIPNV 365
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366 QENGLFSLPYLGSWMLCMILSGPADNLRKNNFTLCVRRIFSLIGMIGPAVLVAAGF 425
384 QSNALLNAVPIYLTWSVGLACALADMLARVITSLNSYKLMNTVASVPSGLIGITY 443
426 ICGDYSLAVAFLTISTTLGGFCGSGSINHLDIABSYAGILGITNTFTATIPSNVP-VI 484
444 VCGDWMVTFVFLMGVSPFGAVVYAGQNMHIALSPRYAGTMTGITSANICGLFAPYVI 503
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504 GLIINRETLTQMHVFLAAGLINGNFTYILFASAEOSMS 546

RESULT 11
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AC OSVDMO;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.

01-MAY-2000, sequence version 1.
 DT 21-FEB-2006, entry version 33.
 DE CG4288-PA, isoform A (CG4288-pb, isoform b) (GH23975p).
 GN ORName=CG4288, Dmel CG4288;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephyridiidae; Drosophilidae; Drosophila.
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 RA MEDLINE=20196006; PubMed=10731132, DOI=10.1126/science.287.5461.2185;
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 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
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 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
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 RL Science 287:2185-2195(2000).
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 RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
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 RT "Finishing a whole-genome shotgun: release 3 of the *Drosophila*
 RT melanogaster euchromatic genome sequence.";
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
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 RA MEDLINE=22426070; PubMed=12537573;
 RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J.W., Svirskas R.,
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 RA Ashburner M., Celniker S.E.;
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
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 RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
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 RA Lewis S.E.;
 RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
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 RP NUCLEOTIDE SEQUENCE.
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 RA Hoskins R., Stapleton M., Pacle J., Park S., Svirskas R., Smith E.,
 RA Yu C., Rubin G.;
 RT "Drosophila melanogaster release 4 sequence.";
 RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
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 RP NUCLEOTIDE SEQUENCE.
 RA Submitted (JAN-2006) to the EMBL/Genbank/DBJ databases.
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 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
 RA Gonzalez M., Guatin H., Li P., Liao G., Miranda A., Mungall C.J.,
 RA Nunoo J., Pacle J., Parasas V., Park S., Pounanavong S., Wan K.,
 RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
 RL Submitted (OCT-2001) to the EMBL/Genbank/DBJ databases.
 CC -!- SUPCELLULAR LOCATION: Membrane; multi-pass membrane protein (By
 CC similarity).
 CC -----
 CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
 CC Distributed under the Creative Commons Attribution-NonCommercial
 CC License
 CC -----
 CC EMBL: AE003730; AAF55770.1; -; Genomic_DNA.
 CC EMBL: AY060776; AAL28324.1; -; mRNA.
 CC EMBL: FBgn0038799; CG4288.
 CC Flybase: FBgn0038799; CG4288.
 CC GO: GO:0005515; F:protein binding; IPI.
 CC InterPro: IPR007114; MFS.
 CC InterPro: IPR011701; MFS_1.
 CC Pfam: PF07690; MFS_1; 1.
 CC PROSITE: PS50850; MFS; 1.
 CC Membrane; Transmembrane; Transport.
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 SQ
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 QY 200 LGVGPFLVLRALDEGLGCVTPRANAMWSSVAPLERSKLISVAGAQGLTVLSLPSG 259
 DB 143 HSLMFLFVKILBGFBSVTPGTHAAWAKSPLESRWASINPAGYVAGIVVAMPESG 202
 QY 260 IICVYMWTVVYFFFGTIGLFWFLMLWTLSVDPQKHRLSHYKEYITLSLRNQLSQX 319
 DB 203 FLATKYGWESVFFVFGTIGVITWLVFVWAGBELDRFSGKECDYIKRTIGVGSQHV 262
 QY 320 SVNPVPLIKSLPLAIVVAHFSYNTWYTLTLTLPYMKELLRNVQENGSLSPYIGS 379
 DB 263 KHPWRAIFTSMPFYAIVASHSEWNGFYTLTLQPSFLRDTLNPDLGKTLISAVPYLAM 322

DR EMBL; Z19153; CAA79549.1; -; Genomic DNA.
 DR PIR; G88553; G88553.
 DR Ensembl; C38C10.2; Caenorhabditis elegans.
 DR WormBase; WBGene00008000; C38C10.2.
 DR WormPep; C38C10.2; CE08647.
 DR InterPro; IPR007114; MFS.
 DR InterPro; IPR011701; MFS_1.
 DR Pfam; PF07690; MFS_1; 1.
 DR PROSITE; PSS0850; MFS; 1.
 KM Complete proteome; Glycoprotein; Hypothetical protein; Ion transport;
 KM Membrane; Sodium; Sodium transport; Symport; Transmembrane; Transport.
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 FT TRANSMEM 112 132 Potential.
 FT TRANSMEM 144 164 Potential.
 FT TRANSMEM 175 195 Potential.
 FT TRANSMEM 205 225 Potential.
 FT TRANSMEM 272 292 Potential.
 FT TRANSMEM 311 331 Potential.
 FT TRANSMEM 348 368 Potential.
 FT TRANSMEM 375 395 Potential.
 FT TRANSMEM 406 426 Potential.
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 FT BINDING 308 308 Phosphopantetheine (covalent)
 FT
 FT CARBOHYD 35 35 (Potential).
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 FT CARBOHYD 69 69 N-linked (GlcNAc...) (Potential).
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 FT CARBOHYD 433 433 N-linked (GlcNAc...) (Potential).
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 Matches 194; Conservative 94; Mismatches 179; Indels 22; Gaps 6;
 QY 55 EESTDTPPLRGAPRAEAAPVCCSARYNLAIFPFQFYIYARVNLVAVMDVDSNTT 114
 DB 2 EGATTPRLVP-----STRALSLVWFPGCLVYVMKRTNNSFAVVCVMEKNT 49
 QY 115 LEDNRSKACPEHSAPDKVHNQTKKYQDAETOGWILGSPFYGIITQIPGVYASKI 174
 DB 50 DTCVEKVRCKCKMTVESNSVIG--EFMDKQTTGCVNLVSFFYGIIGSHLASRY 108
 QY 175 GGRMLLFGILGTAVALTLFTPIADLGVPLIVLRALGEGVTPPAMAMSSVAPPL 234
 DB 109 GGRVAVFTILGSAALLTLNPAARTSEVALILRAIGFLQCATPPAMHTMWSVNGPPL 168
 QY 235 ESKSLISYAGQOLGTIVSLPSGLIICY--MMNTYVYFFGCTIGIFFLLIMLVSD 291
 DB 169 ELSTVLGVYVAGQINIVYVLPISGLICEYFGDGPSPISFYIIGVGVLTAVMAYVSSD 228
 QY 292 TPQKHRIHYEKYLLSRNQLSSQ---KSPVWPILKSLPLMAIVVAHFSYMTFY 347
 DB 229 KATHRPRITPEEKQYIVTAVEASMGKDTGVPTPIKILITSPAVWACNAGHAGMDGAY 288
 QY 348 TLTLTLPTYMKELLRNVQENGFLSLPYGLSWLMLSGQADNLRANKNFSSTLCVRI 407
 DB 289 TMLVSLPSFLKDVLTGNTLSLGAVASIPYLAFLAINAGVADTLRSKQILSTIMTRRA 348
 QY 408 FSLIGMIGPAVLVAAGFTGCDYS-LAVAFLTISTLGGCCSGFSINHLIDIPSTAGIL 466
 DB 349 AMLVALVIGQIFLVASGYCGGDVVIIFITGMAISGIVQVGFVNVYLEIAPPSGTV 408
 QY 467 LGITNFEATIPGVWGVIAKSLTPDNTVGEVQVTFYIAAINVGAIFFTLPKGEVQNW 526
 DB 409 MGTGNTISALAGIISPAVSSYLTNPNGTOEWMVLMITAGILITGALLISIFASGEVQPM 468
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 DB 527 A-LNDHGH 534

DB 469 AKLTAERGH 477
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 ID QY02087_MOUSE
 AC QY02087_MOUSE
 DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
 DT 01-DEC-2001, sequence version 1.
 DT 07-FEB-2006, entry version 25.
 DE Vesicular glutamate transporter 2 (Solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 6).
 GN Name=SLC17a6.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; OC Muroidae; Muridae; Murinae; Mus.
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 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=21453279; PubMed=11432869; DOI=10.1074/jbc.M104578200;
 RA Bai L., Xu H., Collinge J.F., Ghishan F.K.;
 RT "Molecular and functional analysis of a novel neuronal vesicular glutamate transporter.";
 RL J. Biol. Chem. 276:36764-36769 (2001).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Eye;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
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 RA Raha S.S., Loquellano N.B., Peters G.J., Abramson R.D., Muliyil S.J.,
 RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
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 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywicki M.I., Skalek U., Smilun D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Eye;
 RG NIH MGC Project;
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
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 EMBL; AF324864; AAL08941.1; -; mRNA.
 EMBL; BC038375; AAH38375.1; -; mRNA.
 DR Ensembl; ENSMUSG00000030500; Mus musculus.
 DR MGI; MGI:2156052; Slc17a6.
 DR GO; GO:0016021; C:integral to membrane; RCA.
 DR GO; GO:0016020; C:membrane; RCA.
 DR GO; GO:0008021; C:synaptic vesicle; IDA.
 DR GO; GO:0005113; F:1-glutamate transporter activity; IDA.
 DR GO; GO:0005215; F:transporter activity; RCA.
 DR GO; GO:0001504; P:neurotransmitter uptake; IDA.
 DR GO; GO:0006810; P:transport; RCA.
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 DR Pfam; PF07690; MFS_1; 1.
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FT	/label= PKC_phospho_site
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PN	WO200005375-A1.
PD	03-FEB-2000.
PE	22-JUL-1999; 99WO-US016676.
PR	22-JUL-1998; 98US-0093843P.
PA	(UYVA-) UNIV VANDERBILT.
PI	Hellerqvist CG, Fu C;
XX	WPI, 2000-205377/18.
XX	DR N-PSDB; AA250879.
XX	New polynucleotide encoding mammalian receptor for streptococcus toxin,
XX	useful for diagnosis and treatment of, e.g. pneumonia in neonates.
XX	Claim 10; Page 93-95; 109pp; English.
XX	The present sequence is partial human GBS (group B beta-haemolytic
XX	streptococci) toxin receptor (HP55). GBS toxin receptor is an integral

CC	protein-rich seven transmembrane domains. Expression vectors comprising
CC	the coding region can be transformed into host cells to express GBS toxin
CC	receptor and its fragments. Detecting the receptor in tissues is used to
CC	diagnose pathological vasculitis/arthritis, e.g. for detecting cancer
CC	metastases. GBS toxin receptors are useful for treating conditions
CC	associated with pathological angiogenesis or neovascularisation
CC	(specifically cancer, reperfusion injury, scarring during wound healing,
CC	ketooids, chronic inflammation (rheumatoid arthritis or psoriasis) or
CC	neural injury)', and to raise specific antibodies used for treating early
CC	onset diseases. Inhibitors of this receptor are useful for treating
CC	pathological or hypoxia-induced endothelial cell proliferation and
CC	migration
XX	
XX	Sequence 536 AA:
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	Query Match 100.0%; Score 2836; DB 3; Length 536;
	Best Local Similarity 100.0%; Pred. No. 1,98-282;
	Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0
OY	1 MAAGAMTPPPVOPARPGFGSGRRSLLCQYASTPAHVGYMRSPVDLARNDEESTDR 60
DB	1 MAAGAMTPPPVOPARPGFGSGRRSLLCQYASTPAHVGYMRSPVDLARNDEESTDR 60
OY	61 TPLLPGARPRAAAPVCCSARYNLALIAAFGEFFIVALTAVNLSVALVDMVDSNTTLEDRNT 120
DB	61 TPLLPGARPRAAAPVCCSARYNLALIAAFGEFFIVALTAVNLSVALVDMVDSNTTLEDRNT 120
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DB	121 SKACPEHSAPIKYHNHQTCKXYOMPAEQMTLSEFFGVIITIQIPGVYASKIGQMML 180
OY	181 GFGLIGTAVALTTFTPIAADLGVPILIVRALGLEGBGTPEPMAHAMSSMAPLERSKLL 240
DB	181 GFGLIGTAVALTTFTPIAADLGVPILIVRALGLEGBGTPEPMAHAMSSMAPLERSKLL 240
OY	241 SISAQAOLGTVISLPSLGIICYYNMWTVVFYFECTTGIEMFLIMLVSTPTQKHKRIS 300
DB	241 SISAQAOLGTVISLPSLGIICYYNMWTVVFYFECTTGIEMFLIMLVSTPTQKHKRIS 300
OY	301 HYEXEYLSSLRNQSSQSQSVPMVBLKSLPLMAIVVAHFPSYNTTFYTLTLPTYMKEI 360
DB	301 HYEXEYLSSLRNQSSQSQSVPMVBLKSLPLMAIVVAHFPSYNTTFYTLTLPTYMKEI 360
OY	361 LRFNVQENGFLSSLPLYSGWLMIIISGOADNLRAXNNFSTLCYRRIFSLIGMGPAVFL 420
DB	361 LRFNVQENGFLSSLPLYSGWLMIIISGOADNLRAXNNFSTLCYRRIFSLIGMGPAVFL 420
OY	421 VAAGFEGCDVSLAVALITISTTLGGFCSSGSFINHLDAIPSYAGILLGITNTFAITRGWV 480
DB	421 VAAGFEGCDVSLAVALITISTTLGGFCSSGSINHLDAIPSYAGILLGITNTFAITRGWV 480
OY	481 GPVIAASLTPTDNTVGEMQTFYIAAIINVGAIFFTLFAKGEVONMALNDHHGRH 536
DB	481 GPVIAASLTPTDNTVGEMQTFYIAAIINVGAIFFTLFAKGEVONMALNDHHGRH 536
RESULT 2	
AE06518	standard; protein; 536 AA.
ID	AE06518
AC	AE06518;
XX	
XX	16-OCT-2001 (first entry)
DT	
XX	
DE	Human group B beta-haemolytic Streptococci toxin receptor (HP59) protein.
XX	
KW	Human; group B beta-haemolytic Streptococci toxin receptor; GBS; HP59;
KW	Cytotoxic; virulence; antihistaminic; osteopathic; vasotropic;
KW	prevention; attenuation; pathogenic condition; cancer; scar;
KW	wound healing; gliosis; nerve injury; chronic wound; reperfusion injury;
KW	ketooid; rheumatoid arthritis; atherosclerosis; osteoarthritis; psoriasis;
XX	vaccine.

OS	Homo sapiens.
XX	Key
XX	Location/Qualifiers
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XX	49. .63
XX	/label= Hab1_immunogenic_peptide
XX	112. .125
XX	/label= Hab2_immunogenic_peptide
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XX	WO200156598-A2.
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XX	09-AUG-2001.
XX	
XX	02-FEB-2001; 2001WO-US003662.
XX	
XX	02-FEB-2000; 2000US-0179870P.
XX	
XX	(UYVA-) UNIV VANDERBILT.
XX	
XX	Hellegriest CG,
XX	
XX	WPI: 2001-488844/53.
XX	
XX	N-PSDB; AAD10325.
XX	
XX	Preventing or attenuating pathoangiogenic conditions e.g. cancer, chronic
XX	wounds, osteoarthritis, keloids and psoriasis in a mammal, by
XX	administering group B beta-hemolytic Streptococci toxin receptor or its
XX	fragment.
XX	
XX	Claim 4; Page 45-47; 52pp; English.
XX	
XX	The present sequence is full length group B beta-hemolytic Streptococci
XX	(GBS) toxin receptor protein, HP59 from human. The present invention
XX	relates to a method for preventing or attenuating a patho-angiogenic
XX	condition in a mammal which comprises administering to the mammal one or
XX	more GBS toxin receptors or their immunogenic fragments to induce or
XX	maintain an immune response to one of GBS toxin receptors. The method is
XX	useful for preventing or ameliorating pathoangiogenic conditions such as
XX	cancer, scarring during wound healing, gliosis during repair of nerve
XX	injury, chronic wounds, keloids, reperfusion injury, rheumatoid
XX	arthritis, atherosclerosis, osteoarthritis and psoriasis in mammals. The
XX	proteins of the invention are also used as vaccines
XX	
XX	Sequence 536 AA;
XX	
XX	Query Match 100.0%; Score 2836; DB 4; Length 536;
XX	Best Local Similarity 100.0%; Pred. No. 1.8e-282;
XX	Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 MAAGAMPRRVQPARBGGFGLSGRRSLTQVASTPAHVGVWRSPVRLARNDGEESTDR 60
DB	1 MAAGAMPRRVQPARBGGFGLSGRRSLTQVASTPAHVGVWRSPVRLARNDGEESTDR 60
QY	61 TPLPGARPAEAAAPVCCSARNLATIAFFGFEFVYALVNLVSVALVDWDSNTTLEDRRT 120
DB	61 TPLPGARPAEAAAPVCCSARNLATIAFFGFEFVYALVNLVSVALVDWDSNTTLEDRRT 120
QY	121 SKACEPSHAPIKVHNQTKKKYQWDAETQGMWLGSPFYGIITQIPGVYASKIGKMWL 180
DB	121 SKACEPSHAPIKVHNQTKKKYQWDAETQGMWLGSPFYGIITQIPGVYASKIGKMWL 180
QY	181 GFGILGTAVLTLFTPIADLGVGLILVRALEGLEGVTFPPMAHMSWAPPLERSKLL 240
DB	181 GFGILGTAVLTLFTPIADLGVGLILVRALEGLEGVTFPPMAHMSWAPPLERSKLL 240
QY	241 SISVGAQLGTVISPLPSGLIICYNNMTYVFFFGFTIGIFMFLIYMWVSPDQGHKIS 300
DB	241 SISVGAQLGTVISPLPSGLIICYNNMTYVFFFGFTIGIFMFLIYMWVSPDQGHKIS 300
QY	301 HYEKEYILLSRNQLSSQKSVPWVDELKSLPMAIVAHFSYNMFTYTLTLTLLPTVKEI 360

Db	301	HYEEKYLSSLRKQQLSSQSSVPWPLLSLPMLAVVHFSYNTFTTLTLPTTKKEI	360C
Qy	361	LRPNVQENGSLSSLPYLGSMGLCMILSGQAADNLRANKNFTSLCYRRIRFSLGIMGPAVFL	420C
Db	361	LRPNVQENGSLSSLPYLGSMGLCMILSGQAADNLRANKNFTSLCYRRIRFSLGIMGPAVFL	420C
Qy	421	VAAFGICDYSLAVAFLLTISTLLGGFCSSGSFSLNHLDIAPSYAGILLGITTPTATIGMV	480C
Db	421	VAAFGICDYSLAVAFLLTISTLLGGFCSSGSFSLNHLDIAPSYAGILLGITTPTATIGMV	480C
Qy	481	GPVIAKSLTPDNVVGEMQVFVYIAAINVFGLIFPTLPAKGEVQWALNDHGHGRH	536C
Db	481	GPVIAKSLTPDNVVGEMQVFVYIAAINVFGLIFPTLPAKGEVQWALNDHGHGRH	536C
RESULT 3			
AAAY45087	ID	AAAY45087 standard; protein; 495 AA.	
AAAY45087;	AC		
XX	DT	31-MAY-2000 (first entry)	
XX	DE	Partial human GBS toxin receptor (HP55).	
XX	KM	Human GBS toxin receptor; group B beta-haemolytic streptococci; HP55;	
KM	KM	pathological vascularisation; cancer metastases; angiogenesis;	
KM	KM	neovascularisation; reperfusion injury; scarring; keloid;	
KM	KM	chronic inflammation; rheumatoid arthritis; psoriasis; neural injury;	
KM	KM	endothelial cell proliferation; antibacterial; anticancer;	
OS	OS	anti-angiogenic; anti-inflammatory; anti-arthritis; anti-psoriatic.	
OS	OS	Homo sapiens.	
FT	FT	Key	Location/Qualifiers
FT	FT	Region	14..20
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FT	FT	26..30	
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FT	FT	/note= "Region of high hydrophobicity used to design	
FT	FT	antigenic peptide"	
XX	XX	MO200005375-A1.	
PD	PD	03-FEB-2000.	
PF	PF	22-JUL-1999; 99MO-US016676.	
XX	XX	22-JUL-1998; 98US-0093843P.	
XX	XX	(UYVA-) UNIV VANDERBILT.	
XX	XX	Heilerqvist CG, Fu C;	
XX	XX	WPI, 2000-205377/18.	
XX	XX	N-PSDB; AAZ50875.	
XX	XX	New polynucleotide encoding mammalian receptor for streptococcus toxin,	
XX	XX	useful for diagnosis and treatment of, e.g. pneumonia in neonates.	
XX	XX	Claim 9; Page 22; 109pp; English.	
XX	XX	The present sequence is partial human GBS (group B beta-haemolytic	
XX	XX	streptococci) toxin receptor (HP55). GBS toxin receptor is an integral	
XX	XX	protein with seven transmembrane domains. Expression vectors comprising	
XX	XX	the coding region can be transformed into host cells to express GBS toxin	
XX	XX	receptor and its fragments. Detecting the receptor in tissues is used to	
XX	XX	diagnose pathological vascularisation, e.g. for detecting cancer	
XX	XX	metastases. GBS toxin receptors are useful for treating conditions	

CC associated with pathological angiogenesis or neovascularisation
CC (specifically cancer, reperfusion injury, scattering during wound healing,
CC keloids, chronic inflammation (rheumatoid arthritis or psoriasis) or
CC neural injury), and to raise specific antibodies used for treating early
CC onset disease. Inhibitors of this receptor are useful for treating
CC pathological or hypoxia-induced endothelial cell proliferation and
CC migration

XX
SQ Sequence 495 AA;

Query Match 92.4%; Score 2621; DB 3; Length 495;

Best Local Similarity 100.0%; Pred. No. 2.2e-260;

Matches 495; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 SVALVDMVDSNTLLEDRNRTSKACEHSAPIKVHNNOTGKKYQMDAETQMIIGSFYGYI 120
QY 162 ITQIPGGYVASKIGKMLGFGILGTAVALTLFTPIAADLGVPGLIVRALBEGLEGVTFP 221
DB 121 ITQIPGGYVASKIGKMLGFGILGTAVALTLFTPIAADLGVPGLIVRALBEGLEGVTFP 180
QY 222 AMHAMSSWAPPLERSKLSISYAGQGTIVISLPISGLIICYMMNTYVYFFGTIGIFW 281
DB 181 AMHAMSSWAPPLERSKLSISYAGQGTIVISLPISGLIICYMMNTYVYFFGTIGIFW 240
QY 282 FLIMWLVSDDTPQKHRIKSHYEKEYILSLRNQLSQKSVPMWPIILKSLPLMAIVVAHFS 341
DB 241 FLIMWLVSDDTPQKHRIKSHYEKEYILSLRNQLSQKSVPMWPIILKSLPLMAIVVAHFS 300
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QY 462 YAGILGINTNTFATIPGMGVPVIAKSLTPDNTVGEMQTVFYIAAIVNFGAIFFTLPAKG 521
DB 421 YAGILGINTNTFATIPGMGVPVIAKSLTPDNTVGEMQTVFYIAAIVNFGAIFFTLPAKG 480
QY 522 EVQNMALNDHHGHRH 536
DB 481 EVQNMALNDHHGHRH 495
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RESULT 4

AAB66967 standard; protein; 495 AA.

AC AAB66967;

DT 18-APR-2001 (first entry)

DE Human AST.

XX Human; AST; noctropic; immunotropic; gene therapy; Salla disease;

KM anion and sugar transporter; anion-cation symporter;

OS Homo sapiens.

PN EPI069184-A1.

PD 17-JAN-2001.

PF 16-JUL-1999; 99EP-00202341.

XX

PR 16-JUL-1999; 99EP-00202341.

XX (ALKU) AKZO NOBEL NV.

XX WPI; 2001-193090/20.

DR N-PSDB; AAF55900.

XX New human transporter gene implicated in Salla disease and lysosomal

PT static acid transport, useful in assays for identifying new drugs, or

PT diagnosing static acid transport defects related to mutations in the

PT transporter gene.

XX Claim 1; Page 10-12; 20pp; English.

XX The present sequence is human Anion and Sugar Transporter (AST) protein

CC sequence. AST has significant homology with several members of the anion-

CC cation symporter (ACS) family of transporters. AST is implicated in Salla

CC disease, and is useful in screening assays for identifying new drugs.

CC Compounds identified via AST screening is useful for preparing a

CC pharmaceutical suitable as an activator or inhibitor of a static acid

CC transporter protein. The pharmaceutical may be used in static acid

CC associated diseases and CNS/immune related disorders

SQ Sequence 495 AA;

Query Match 92.4%; Score 2621; DB 4; Length 495;

Best Local Similarity 100.0%; Pred. No. 2.2e-260;

Matches 495; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 42 MRSPPVDLARNDEESTDRTPLPGAPRAEAPVCCSARYNLAIALAFGFFIVYALRVNL 101
DB 1 MRSPPVDLARNDEESTDRTPLPGAPRAEAPVCCSARYNLAIALAFGFFIVYALRVNL 60
QY 102 SVALVDMVDSNTLLEDRNRTSKACEHSAPIKVHNNOTGKKYQMDAETQMIIGSFYGYI 161
DB 61 SVALVDMVDSNTLLEDRNRTSKACEHSAPIKVHNNOTGKKYQMDAETQMIIGSFYGYI 120
QY 162 ITQIPGGYVASKIGKMLGFGILGTAVALTLFTPIAADLGVPGLIVRALBEGLEGVTFP 221
DB 121 ITQIPGGYVASKIGKMLGFGILGTAVALTLFTPIAADLGVPGLIVRALBEGLEGVTFP 180
QY 222 AMHAMSSWAPPLERSKLSISYAGQGTIVISLPISGLIICYMMNTYVYFFGTIGIFW 281
DB 181 AMHAMSSWAPPLERSKLSISYAGQGTIVISLPISGLIICYMMNTYVYFFGTIGIFW 240
QY 282 FLIMWLVSDDTPQKHRIKSHYEKEYILSLRNQLSQKSVPMWPIILKSLPLMAIVVAHFS 341
DB 241 FLIMWLVSDDTPQKHRIKSHYEKEYILSLRNQLSQKSVPMWPIILKSLPLMAIVVAHFS 300
QY 342 YNMTFYTLTLPTWKKEILRFNVQENGFLSSLPYLGSWLCLMISGQAADNLRKWNFST 401
DB 301 YNMTFYTLTLPTWKKEILRFNVQENGFLSSLPYLGSWLCLMISGQAADNLRKWNFST 360
QY 402 LCVRRIFFSLIGMIGPAFLVAAGFICDYSLVAFLITSTLGGFCSSGFSINHLDIAPS 461
DB 361 LCVRRIFFSLIGMIGPAFLVAAGFICDYSLVAFLITSTLGGFCSSGFSINHLDIAPS 420
QY 462 YAGILGINTNTFATIPGMGVPVIAKSLTPDNTVGEMQTVFYIAAIVNFGAIFFTLPAKG 521
DB 421 YAGILGINTNTFATIPGMGVPVIAKSLTPDNTVGEMQTVFYIAAIVNFGAIFFTLPAKG 480
QY 522 EVQNMALNDHHGHRH 536
DB 481 EVQNMALNDHHGHRH 495
```

RESULT 5

ADJ75516 standard; protein; 495 AA.

AC ADJ75516;

DT 20-MAY-2004 (first entry)

XX

XX Marker gene related amino acid sequence SEQ ID NO:768.
 DE bronchial asthma; chronic obstructive pulmonary disease;
 KM respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;
 KM gene therapy; marker.
 XX Homo sapiens.
 OS
 PN EP1394274-A2.
 XX
 PD 03-MAR-2004.
 XX
 PF 04-AUG-2003; 2003EP-00254857.
 XX
 PR 06-AUG-2002; 2002JP-00229312.
 PR 20-MAR-2003; 2003JP-00077212.
 XX
 PA (GENO-) GENOX RES INC.
 PI Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuhara K;
 XX WPI; 2004-193155/19.
 DR
 XX Testing for bronchial asthma or chronic obstructive pulmonary disease by
 PT comparing the expression level of a marker gene in a biological sample
 PT from a subject with the expression level of the gene in a sample from a
 PT healthy subject.
 XX
 PS Example 11; SEQ ID NO 768; 241pp; English.
 XX
 CC The present invention describes a method of testing for bronchial asthma
 CC or chronic obstructive pulmonary disease. The method comprises
 CC determining the expression level of a marker gene in a biological sample
 CC from a subject, comparing the expression level determined with the
 CC expression level of the marker gene in a biological sample from a healthy
 CC subject, and judging whether the subject has bronchial asthma or chronic
 CC obstructive pulmonary disease. The marker gene comprises: (a) a group of
 CC genes (S1) whose expression levels increase when respiratory epithelial
 CC cells are stimulated with interleukin-13; or (b) a group of genes (S2)
 CC whose expression levels decrease when respiratory epithelial cells are
 CC stimulated with interleukin-13. Also described: (1) a reagent (I) for
 CC testing for bronchial asthma or chronic obstructive pulmonary disease;
 CC (2) a kit for screening for a candidate compound for a therapeutic agent
 CC to treat bronchial asthma or chronic obstructive pulmonary disease; (3)
 CC an animal model for bronchial asthma or chronic obstructive pulmonary
 CC disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a
 CC method for producing an animal model for bronchial asthma or chronic
 CC obstructive pulmonary disease; (6) a therapeutic agent for bronchial
 CC asthma or chronic obstructive pulmonary disease, comprising the compound,
 CC a marker gene or an antisense nucleic acid corresponding to a portion of
 CC the marker gene, a ribozyme, a polynucleotide that suppresses the
 CC expression of the gene through an RNAi effect or an antibody recognising
 CC a protein encoded by a marker gene; and (7) a DNA chip for testing for
 CC bronchial asthma or a chronic obstructive pulmonary disease, on which a
 CC probe has been immobilised to assay a marker gene. (1) has respiratory
 CC and antiasthmatic activities, and can be used in gene therapy. The method
 CC is useful for testing for or screening for a therapeutic agent for
 CC bronchial asthma or chronic obstructive pulmonary disease. The present
 CC sequence is used in the exemplification of the present invention.
 XX
 SQ Sequence 495 AA;
 Query Match 92.4%; Score 2621; DB 8; Length 495;
 Best Local Similarity 100.0%; Pied. No. 2,2e-260;
 Matches 495; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 42 MRSPVRLARNDSSESTDRTPLLPGAPRAEAPVCCSARYVLTALTFGPFIVALKVNL 101
 DB 1 MRSVRLARNDSSESTDRTPLLPGAPRAEAPVCCSARYVLTALTFGPFIVALKVNL 60
 QY 102 SVALVDMVDSNTLTEDNRTSKACEHSAPIKVHNQGTCKYQMDAETQWILGSPFYGYI 161

DB 61 SVALVDMVDSNTLTEDNRTSKACEHSAPIKVHNQGTCKYQMDAETQWILGSPFYGYI 120
 QY 162 ITQIPGVYASKIGKGMILGFIQTAVLTLFTPIADLGVGPHIVLRALGLEGVTFP 221
 DB 121 ITQIPGVYASKIGKGMILGFIQTAVLTLFTPIADLGVGPHIVLRALGLEGVTFP 180
 QY 222 AMHAMSSWAPPLERSKILSISVAGQIGTVISLPLSGIICYNMWTYVFFFGTIGIFW 281
 DB 181 AMHAMSSWAPPLERSKILSISVAGQIGTVISLPLSGIICYNMWTYVFFFGTIGIFW 240
 QY 282 FLMTIMVSDTPQCHKRISHYKEYIILSLNQLSSQKSVWVPLKSLPLMAIVVAHFS 341
 DB 241 FLMTIMVSDTPQCHKRISHYKEYIILSLNQLSSQKSVWVPLKSLPLMAIVVAHFS 300
 QY 342 YNMFTFTLLTLPTPYMEIILFENVQENGFLSSLPYLSGMLCMISGQADNLRKMNST 401
 DB 301 YNMFTFTLLTLPTPYMEIILFENVQENGFLSSLPYLSGMLCMISGQADNLRKMNST 360
 QY 402 LCVRRIFSLIGMIGPAVFLVAGFICGDSLAVALFTISTTLGFCSSGFSINHLDIAPS 461
 DB 361 LCVRRIFSLIGMIGPAVFLVAGFICGDSLAVALFTISTTLGFCSSGFSINHLDIAPS 420
 QY 462 YAGILLGITNTFATITPGWGVPIAKSLTPDNTVGSEMQTFYIAAINVFGAIFPTLPFKG 521
 DB 421 YAGILLGITNTFATITPGWGVPIAKSLTPDNTVGSEMQTFYIAAINVFGAIFPTLPFKG 480
 QY 522 EVQNWALNDHGHHRH 536
 DB 481 EVQNWALNDHGHHRH 495
 RESULT 6
 ADR14587
 ID ADR14587 standard; protein; 495 AA.
 AC ADR14587;
 XX 21-OCT-2004 (first entry)
 DE Human NF-kappaB pathway-associated protein SeqID588.
 XX
 KM NF-kappaB pathway; antiinflammatory; cytosolic; hepatotropic; virucide;
 KM antiatheritic; antirheumatic; gastrointestinal-Gen; antiasthmatic;
 KM antiatherosclerotic; immunomodulator; cerebroprotective; vasotropic;
 KM immunosuppressive; vunerary; gene therapy; immune disorder;
 KM inflammatory disorder; Hodgkin's lymphoma; haematopoietic tumour;
 KM hepatic disorder; hypohidrotic ectodermal dysplasia;
 KM hyper-IGM syndrome; hypohidrotic ectodermal dysplasia;
 KM X-linked anhidrotic ectodermal dysplasia; immunodeficiency;
 KM viral infection; HIV-1; HTLV-1; hepatitis B; hepatitis C; EBV; influenza;
 KM viral replication; host cell survival; evasion of immune response;
 KM rheumatoid arthritis; inflammatory bowel disease; colitis; asthma;
 KM atherosclerosis; cachexia; euthyroid sick syndrome; stroke; EAE;
 KM autoimmune disorder; hyper immune activity;
 KM aberrant acute phase response; hypercongenital condition; birth defect;
 KM necrotic lesion; wound; organ transplant rejection;
 KM aberrant signal transduction; proliferating disorder; cancer;
 KM HIV propagation; human.
 XX
 OS Homo sapiens.
 OS
 PN WO2004065577-A2.
 XX
 PD 05-AUG-2004.
 XX
 PF 13-JAN-2004; 2004WO-US000798.
 XX
 PR 14-JAN-2003; 2003US-0440068P.
 PR 12-MAY-2003; 2003US-0469757P.
 XX
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 PI Nadler SG, Neubauer MG, Feder JN, Carman J;

XX WPI, 2004-562168/54.
 DR N-PSDB; ADRL4586.
 XX
 PT New isolated polynucleotides and polypeptides associated with NF-kappa
 PT pathway, useful for diagnosing, treating, or preventing disorders or
 PT diseases associated with NF-kappa pathway.
 XX
 PS Claim 6; SEQ ID NO 588; 237bp; English.
 XX
 CC This invention relates to the novel association of protein sequences (and
 CC the genes which encode them) to the NF-kappa pathway. The invention may
 CC be useful for the production of compounds with an antiinflammatory,
 CC cytostatic, hepatotropic, virucide, antiarthritic, antirheumatic,
 CC gastrointestinal-Gen, antiaesthetic, antiarteriosclerotic,
 CC immunomodulator, cerebroprotective, vasotropic, immunosuppressive or
 CC vulnerary activity or for gene therapy. The proteins and nucleotides are
 CC useful for diagnosing, preventing, treating, or ameliorating conditions
 CC or diseases associated with the NF-kappa pathway. The condition is an
 CC immune disorder, an inflammatory disorder, cancer, aberrant apoptosis,
 CC related to aberrant NF-kappa regulation, cancer, aberrant apoptosis,
 CC hepatic disorders, Hodgkin's lymphomas, haematopoietic tumours, hyper-IgM
 CC syndromes, hypohidrotic ectodermal dysplasia, X-linked anhidrotic
 CC ectodermal dysplasia, immunodeficiency, viral infections, HIV-1, HTLV-1,
 CC hepatitis B, hepatitis C, EBV, influenza, viral replication, host cell
 CC survival, evasion of immune responses, rheumatoid arthritis, inflammatory
 CC bowel disease, colitis, asthma, atherosclerosis, cachexia, euthyroid sick
 CC syndrome, stroke, EAE, autoimmune disorders, disorders related to hyper
 CC immune activity, disorders related to aberrant acute phase responses,
 CC hypercongenital conditions, birth defects, necrotic lesions, wounds,
 CC organ transplant rejection, conditions related to organ transplant
 CC rejection, disorders related to aberrant signal transduction,
 CC proliferating disorders, cancers and HIV propagation in cells infected
 CC with other viruses. The present sequence is that of a human protein which
 CC is subject to the novel association with the NF-kappa pathway of the
 CC invention. Note: This sequence does not appear in the specification but
 CC was obtained by the indexer from Genbank.
 XX
 XX Sequence 495 AA;
 SQ
 Query Match 92.4%; Score 2621; DB 8; Length 495;
 Best Local Similarity 100.0%; Pred. No. 2, 2e-260;
 Matches 495; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 MRSPPVRLANDGEESTDRTPFLPGAPRAEAPVCCSARXYLALAFPGFIVYALRVNL 101
 DB 1 MRSPPVRLANDGEESTDRTPFLPGAPRAEAPVCCSARXYLALAFPGFIVYALRVNL 60
 QY 102 SVALLVMDVDSNTTLEDNRTSKACPEHSAPIKVHNNGKKYQWMAEQGWLGSFFGYI 161
 DB 61 SVALLVMDVDSNTTLEDNRTSKACPEHSAPIKVHNNGKKYQWMAEQGWLGSFFGYI 120
 QY 162 ITOIPGVYVASKIGKMLGFGILGTAVLTLFTPIADLGVPLIVLRALGLEGVTFP 221
 DB 121 ITOIPGVYVASKIGKMLGFGILGTAVLTLFTPIADLGVPLIVLRALGLEGVTFP 180
 QY 222 AMHAMSSWAPPLERSKILSTSYAGQGLGVYISPLSGITYYVNMWYVFFPFGTIGFW 281
 DB 181 AMHAMSSWAPPLERSKILSTSYAGQGLGVYISPLSGITYYVNMWYVFFPFGTIGFW 240
 QY 282 FLMIWIVSDTPQGHKRIHSEKEYIISLNNOSSQSVWVILKSLPMAIVVAHFS 341
 DB 341 FLMIWIVSDTPQGHKRIHSEKEYIISLNNOSSQSVWVILKSLPMAIVVAHFS 300
 QY 342 YNMFTYTLTLPTYNKEILRFNVQENGFLSSLPYLGSWLCMLISGQADNWRKWNFST 401
 DB 301 YNMFTYTLTLPTYNKEILRFNVQENGFLSSLPYLGSWLCMLISGQADNWRKWNFST 360
 QY 402 LCVARIFSLIGMIGPAAFLVAAFGTICDYSIAVAFITSTLUGFGCSGSGSINHLDIAPS 461
 DB 361 LCVARIFSLIGMIGPAAFLVAAFGTICDYSIAVAFITSTLUGFGCSGSGSINHLDIAPS 420
 QY 462 YAGILGITNTFATIPGMVGPVIAKSLTPDNTVGEWQVFYIAAIVFGAIFTLFAKG 521

DB 421 YAGILGITNTFATIPGMVGPVIAKSLTPDNTVGEWQVFYIAAIVFGAIFTLFAKG 480
 QY 522 EYONWALNDHGHGRH 536
 DB 481 EYONWALNDHGHGRH 495
 RESULT 7
 ID ADP25217 standard; protein; 495 AA.
 XX
 AC ADP25217;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE PRO polypeptide SEQ ID NO:2395.
 XX
 XX PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive;
 KW osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic;
 KW antiaesthetic; hepatotropic; respiratory; gene therapy; immune system.
 XX
 OS Unidentified.
 XX
 PN WC2004041170-A2.
 XX
 PD 21-MAY-2004.
 XX
 PF 30-OCT-2003; 2003WC-US034312.
 XX
 PR 01-NOV-2002; 2002US-0423394P.
 XX
 PA (GENTH) GENENTECH INC.
 XX
 PI Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI;
 PI Wu TD;
 XX
 DR N-PSDB; ADP25216.
 XX
 PT WPI, 2004-419628/39.
 XX
 PT New PRO polypeptides and polynucleotides, useful for treating e.g.
 PT erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated
 PT renal disease, or demyelinating diseases of the central or peripheral
 PT nervous system.
 XX
 PS Claim 7; SEQ ID NO 2395; 2940bp; English.
 XX
 CC The invention relates to a novel isolated nucleic acid and the PRO
 CC polypeptide encoded by it. A protein of the invention has
 CC antiinflammatory, antiarthritic, antirheumatic, immunosuppressive,
 CC osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic,
 CC antiaesthetic, hepatotropic, and respiratory activity. A polynucleotide
 CC of the invention may have a use in gene therapy. The PRO polypeptide, its
 CC agonist, antagonist, or antibody that specifically binds to the
 CC polypeptide is useful for treating an immune related disorder such as
 CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
 CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an
 CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
 CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
 CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal
 CC disease, a demyelinating disease of the central or peripheral nervous
 CC system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,
 CC a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary
 CC disease, infectious or autoimmune chronic active hepatitis, primary
 CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
 CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
 CC disease, an autoimmune or immune-mediated skin disease, a bullous skin
 CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
 CC disease, asthma, allergic rhinitis, atopic dermatitis, food
 CC hypersensitivity, urticaria, an immunologic disease of the lung,
 CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
 CC pneumonitis, a transplantantion associated disease, graft rejection or
 CC graft-versus-host disease. The present sequence represents a PRO protein

CC of the invention.
XX
SQ Sequence 495 AA;

Query Match 92.4%; Score 2621; DB 8; Length 495;
Best Local Similarity 100.0%; Pred. No. 2.2e-260;
Matches 495; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 42 MRSFVRDLARNDESESTDRTPLLPGAPRAEAPVCCSARNYLAIALAFGFPIYALRVNL 101
DB 1 MRSFVRDLARNDESESTDRTPLLPGAPRAEAPVCCSARNYLAIALAFGFPIYALRVNL 60
QY 102 SVALVDVDSNTLTLEDNRTSKACEHSAPIKVHHNQTGKKYQMDAETQGMILGSFFYGYI 161
DB 61 SVALVDVDSNTLTLEDNRTSKACEHSAPIKVHHNQTGKKYQMDAETQGMILGSFFYGYI 120
QY 162 ITQIPGGYVASKIGKKMLGFGILGTAVLTLFPIAADLGVGPLIVRALEGEGVTFP 221
DB 121 ITQIPGGYVASKIGKKMLGFGILGTAVLTLFPIAADLGVGPLIVRALEGEGVTFP 180
QY 222 AMHAMSSWAPPLERSKULSISYAGAOIGTVISLPLSGIICVYNNMTYVFYFPGTIGIFW 281
DB 181 AMHAMSSWAPPLERSKULSISYAGAOIGTVISLPLSGIICVYNNMTYVFYFPGTIGIFW 240
QY 282 FLMIWLVSDTPQKHKRISHYEKEYILSLRNQLSOKSPWVPILKSLPLMAIVVAHFS 341
DB 241 FLMIWLVSDTPQKHKRISHYEKEYILSLRNQLSOKSPWVPILKSLPLMAIVVAHFS 300
QY 342 YNNTFYTLTLTLPTYMKEILRFNVQENGFLSSLPYIGSWLCLMILSGAADNLRANKNFST 401
DB 301 YNNTFYTLTLTLPTYMKEILRFNVQENGFLSSLPYIGSWLCLMILSGAADNLRANKNFST 360
QY 402 LCVRRIFSLIGMIGPAFLVAAGFIGDYSIAVAFLTISTTLGFCSSGSGFINHLDIAPS 461
DB 361 LCVRRIFSLIGMIGPAFLVAAGFIGDYSIAVAFLTISTTLGFCSSGSGFINHLDIAPS 420
QY 462 YAGILGINTTFATIPGMVGPVIAKSLTPDNTVGEMQTVFYIAAINVFGAIFFTLPFAKG 521
DB 421 YAGILGINTTFATIPGMVGPVIAKSLTPDNTVGEMQTVFYIAAINVFGAIFFTLPFAKG 480
QY 522 EVQNMALNDHGHHRH 536
DB 481 EVQNMALNDHGHHRH 495

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RESULT 8
AAM38959
ID AAM38959 standard; protein; 495 AA.

XX AAM38959;
AC AAM38959;
XX
DT 22-OCT-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 2104.
XX
KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemoglobin; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200153312-A1.
XX
PD 26-JUL-2001.
XX
PF 26-DEC-2000; 2000WO-US034263.
XX
PR 23-DEC-1999; 99US-00471275.
PR 21-JAN-2000; 2000US-00488725.
PR 25-APR-2000; 2000US-0052317.

PR 20-JUN-2000; 2000US-00598042.
PR 19-JUL-2000; 2000US-00620312.
PR 03-AUG-2000; 2000US-00653450.
PR 14-SEP-2000; 2000US-00662191.
PR 19-OCT-2000; 2000US-00693036.
PR 29-NOV-2000; 2000US-00727344.

(HYSE-) HYSEQ INC.

PA Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D,
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AD, Yang Y, Zhang J, Zhao QA,
PI Zhou P, Goodrich R, Drmanac RT;

DR WPI; 2001-442253/47.
DB N-PSDB; AA158115.

PT Novel nucleic acids and polypeptides, useful for treating disorders such
PT as central nervous system injuries.

PS Example 3; SEQ ID NO 2104; 10078pp; English.

CC The invention relates to human nucleic acids (AA157798-AA161365) and the
CC encoded polypeptides (AAM38642-AA42213) with nootropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC facilitation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemia and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification

XX Sequence 495 AA;

Query Match 92.2%; Score 2614; DB 4; Length 495;
Best Local Similarity 99.8%; Pred. No. 1.2e-259;
Matches 494; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 42 MRSFVRDLARNDESESTDRTPLLPGAPRAEAPVCCSARNYLAIALAFGFPIYALRVNL 101
DB 1 MRSFVRDLARNDESESTDRTPLLPGAPRAEAPVCCSARNYLAIALAFGFPIYALRVNL 60
QY 102 SVALVDVDSNTLTLEDNRTSKACEHSAPIKVHHNQTGKKYQMDAETQGMILGSFFYGYI 161
DB 61 SVALVDVDSNTLTLEDNRTSKACEHSAPIKVHHNQTGKKYQMDAETQGMILGSFFYGYI 120
QY 162 ITQIPGGYVASKIGKKMLGFGILGTAVLTLFPIAADLGVGPLIVRALEGEGVTFP 221
DB 121 ITQIPGGYVASKIGKKMLGFGILGTAVLTLFPIAADLGVGPLIVRALEGEGVTFP 180
QY 222 AMHAMSSWAPPLERSKULSISYAGAOIGTVISLPLSGIICVYNNMTYVFYFPGTIGIFW 281
DB 181 AMHAMSSWAPPLERSKULSISYAGAOIGTVISLPLSGIICVYNNMTYVFYFPGTIGIFW 240
QY 282 FLMIWLVSDTPQKHKRISHYEKEYILSLRNQLSOKSPWVPILKSLPLMAIVVAHFS 341
DB 241 FLMIWLVSDTPQKHKRISHYEKEYILSLRNQLSOKSPWVPILKSLPLMAIVVAHFS 300
QY 342 YNNTFYTLTLTLPTYMKEILRFNVQENGFLSSLPYIGSWLCLMILSGAADNLRANKNFST 401
DB 301 YNNTFYTLTLTLPTYMKEILRFNVQENGFLSSLPYIGSWLCLMILSGAADNLRANKNFST 360
QY 402 LCVRRIFSLIGMIGPAFLVAAGFIGDYSIAVAFLTISTTLGFCSSGSGFINHLDIAPS 461
DB 361 LCVRRIFSLIGMIGPAFLVAAGFIGDYSIAVAFLTISTTLGFCSSGSGFINHLDIAPS 420
QY 462 YAGILGINTTFATIPGMVGPVIAKSLTPDNTVGEMQTVFYIAAINVFGAIFFTLPFAKG 521

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Db	Accession	Protein Name	Protein Description
Db	421	YAGILIGTNTFATLPGWGVPIANSKLTDPNTVGEQVTFYIAAIAINFGAIFPTLPK	460
Oy	522	EVQNMALNDHGHRRH	536
Db	461	EVQNMALNDHGHRRH	495
RESULT 9			
ID	AAV45088	standard: protein; 495 AA.	
XX	AAV45088;		
XX			
DT	31-MAY-2000	(first entry)	
XX			
DE	Sheep GBS toxin receptor (SP55).		
XX			
KW	Sheep GBS toxin receptor; group B beta-haemolytic streptococci; SP55;		
KW	pathological vasculaturation; cancer metastases; angiogenesis; sheep;		
KW	neovascularisation; reperfusion injury; scarring; keloid;		
KW	chronic inflammation; rheumatoid arthritis; psoriasis; neural injury;		
KM	endothelial cell proliferation; antibacterial; anticancer;		
KM	anti-angiogenic; anti-inflammatory; anti-arthritis; anti-psoriatic.		
XX			
OS	Ovis sp.		
XX			
XX			
Key	Location/Qualifiers		
FT	Peptide	7..22	/label= P55a
FT		/note= "Immunogenic peptide"	
FT		8..35	/label= P56a
FT	Peptide	/note= "Immunogenic peptide"	
FT		11..14	/label= CK2.phospho.site
FT	Modified-site	/note= "Predicted phosphorylation site"	
FT		17..19	/label= PKC.phospho.site
FT	Modified-site	/note= "Predicted phosphorylation site"	
FT		37..39	/label= PKC.phospho.site
FT	Modified-site	/note= "Predicted phosphorylation site"	
FT		42..58	/note= "Predicted transmembrane domain"
FT	Domain	55..57	/label= PKC.phospho.site
FT	Modified-site	/note= "Predicted phosphorylation site"	
FT		59..62	/note= "asn is N-glycosylated"
FT	Modified-site	71..84	/label= P57a
FT	Peptide	/note= "Immunogenic peptide"	
FT		71..74	/note= "asn is N-glycosylated"
FT	Modified-site	73..76	/label= CK2.phospho.site
FT	Modified-site	/note= "Predicted phosphorylation site"	
FT		73..75	/label= PKC.phospho.site
FT	Modified-site	/note= "Predicted phosphorylation site"	
FT		77..80	/note= "asn is N-glycosylated"
FT	Modified-site	79..82	/label= CK2.phospho.site
FT	Modified-site	/note= "Predicted phosphorylation site"	
FT		95..98	/note= "asn is N-glycosylated"
FT	Modified-site	97..100	/note= "Putative amidation site"
FT	Modified-site	97..99	/label= PKC.phospho.site
FT	Modified-site	/note= "Predicted phosphorylation site"	
FT		126..131	

FT		/note= "Predicted myristylation site"
FT	Domain	135. .157
FT	/note= "Outer boundary of transmembrane domain"	137. .153
FT	Domain	137. .153
FT	/note= "Inner boundary of transmembrane domain"	142. .147
FT	Modified-site	142. .147
FT	/note= "Predicted myristylation site"	162. .167
FT	Modified-site	162. .167
FT	/note= "Predicted myristylation site"	172. .177
FT	Modified-site	172. .177
FT	/note= "Predicted myristylation site"	205. .210
FT	Modified-site	205. .210
FT	/note= "Predicted myristylation site"	209. .214
FT	Modified-site	209. .214
FT	/note= "Predicted myristylation site"	225. .228
FT	Modified-site	225. .228
FT	/note= "Aen is N-glycosylated"	226. .252
FT	Domain	226. .252
FT	/note= "Outer boundary of transmembrane domain"	232. .248
FT	Domain	232. .248
FT	/note= "Inner boundary of transmembrane domain"	254. .256
FT	Modified-site	254. .256
FT	/label= PKC phospho site	259. .262
FT	Modified-site	259. .262
FT	/label= CR2 phospho site	269. .271
FT	Modified-site	269. .271
FT	/note= "Predicted phosphorylation site"	276. .278
FT	Modified-site	276. .278
FT	/label= PKC phospho site	302. .305
FT	Modified-site	302. .305
FT	/note= "Predicted phosphorylation site"	328. .345
FT	Domain	328. .345
FT	/note= "Outer boundary of transmembrane domain"	328. .344
FT	Domain	328. .344
FT	/note= "Inner boundary of transmembrane domain"	337. .342
FT	Modified-site	337. .342
FT	/note= "Predicted myristylation site"	357. .360
FT	Modified-site	357. .360
FT	/note= "Aen is N-glycosylated"	365. .389
FT	Domain	365. .389
FT	/note= "Outer boundary of transmembrane domain"	369. .385
FT	Domain	369. .385
FT	/note= "Inner boundary of transmembrane domain"	386. .391
FT	Modified-site	386. .391
FT	/note= "Predicted myristylation site"	390. .407
FT	Domain	390. .407
FT	/note= "Outer boundary of transmembrane domain"	390. .406
FT	Domain	390. .406
FT	/note= "Inner boundary of transmembrane domain"	403. .408
FT	Modified-site	403. .408
FT	/note= "Predicted myristylation site"	423. .428
FT	Modified-site	423. .428
FT	/note= "Predicted myristylation site"	427. .432
FT	Modified-site	427. .432
FT	/note= "Predicted myristylation site"	452. .455
FT	Modified-site	452. .455
FT	/label= PKC phospho site	456. .479
FT	Domain	456. .479
FT	/note= "Predicted phosphorylation site"	458. .474
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PR 22-JUN-1998; 98US-0093843P.
 XX (UYVA-) UNIV VANDERBILT.
 XX
 PI Hellerqvist CG, Fu C;
 XX
 DR WPI; 2000-205377/18.
 DR N-PSDB; AA250876.
 XX
 PT New polynucleotide encoding mammalian receptor for streptococcus toxin,
 PT useful for diagnosis and treatment of, e.g. pneumonia in neonates.
 XX
 PS Claim 10; Page 22; 109pp; English.
 XX
 CC The present sequence is sheep GBS (group B beta-haemolytic streptococci)
 CC toxin receptor (SP55). Sheep GBS toxin receptor is an integral protein
 CC with seven transmembrane domains. Expression vectors comprising the
 CC coding region can be transformed into host cells to express GBS toxin
 CC receptor and its fragments. Detecting the receptor in tissues is used to
 CC diagnose pathological vascularisation, e.g. for detecting cancer
 CC metastases. GBS toxin receptors are useful for treating conditions
 CC associated with pathological angiogenesis or neovascularisation
 CC (specifically cancer, reperfusion injury, scarring during wound healing,
 CC keloids, chronic inflammation (rheumatoid arthritis or psoriasis) or
 CC neural injury), and to raise specific antibodies used for treating early
 CC onset disease. Inhibitors of this receptor are useful for treating
 CC pathological or hypoxia-induced endothelial cell proliferation and
 CC migration
 CC
 SQ Sequence 495 AA;
 Query Match 82.1%; Score 2329; DB 3; Length 495;
 Best Local Similarity 86.3%; Pred. No. 2.6e-230;
 Matches 427; Conservative 39; Mismatches 29; Indels 0; Gaps 0;
 QY 42 MRSVVDLARNDEESTDRPLPGAPRAEAPVCCSARNYLAIAFFGFIVYALRYNL 101
 DB 1 MRSVPSDLAPSDGEGSDRTPLORAPRABAPVCCSARNYLAIAFFGFIVYALRYNL 60
 QY 102 SVALLVDVDSSTLTEDNRTSKACEPSHAPIRVHNQTKQOMAEOTGWLGSFFPYXI 161
 DB 61 SVALLVDVDSSTLTAKNRTSYECASHAPIRVHNQTKKRYMAETGWLGSFFPYXI 120
 QY 162 ITQIPGGVASKIGKMLGFGIIGTAVLTFTPLAADLGVGPIVLRALEGEGVTEP 221
 DB 121 ITQIPGGVASKIGKMLGFGIIGTAVLTFTPLAADLGVGPIVLRALEGEGVTEP 180
 QY 222 AMHAMSSWAPPLERSKLLSISVAGAOIGTVISLPLSGIICYYNMWTVFFYFCTIGIFW 281
 DB 181 AMHAMSSWAPPLERSKLLSISVAGAOIGTVISLPLSGIICYYNMWTVFFYFCTIGIFW 240
 QY 282 FLMLMVLVSDTPQGHKASHYKEYIISLBNQISSQKSVWVPLKSLPLMAIVVAHS 341
 DB 241 FLMLMVLVSDTPQGHKASHYKEYIISLBNQISSQKSVWVPLKSLPLMAIVVAHS 300
 QY 342 YNMTFTYLLTLLPTYMKELIRENVOENGFLSLPYLGSMLCMLISGQADNLRKMNST 401
 DB 301 YNMTFTYLLTLLPTYMKELIRENVOENGFLSLPYLGSMLCMLISGQADNLRKMNST 360
 QY 402 LCVARISLSLIGMIPAVFLVAGFICGDYSIAVAFLTISTTLGFGCSGSGFINHDIAPS 461
 DB 361 LCVARISLSLIGMIPAVFLVAGFICGDYSIAVAFLTISTTLGFGCSGSGFINHDIAPS 420
 QY 462 YAGILGITYTFAITPBGWGPVIAKSLTPDVTGEMQVFIYAAINVEGAIFFTLPAKG 521
 DB 421 YAGILGITYTFAITPBGWGPVIAKSLTPDVTGEMQVFIYAAINVEGAIFFTLPAKG 480
 QY 522 EVQNMALNDHGRHRH 536
 DB 481 EVQNMALNDHGRHRH 495

AAE06519
 ID AAE06519 standard; protein; 495 AA.
 XX
 AC AAE06519;
 XX
 DT 16-OCT-2001 (first entry)
 XX
 DE Sheep group B beta-haemolytic Streptococci toxin receptor (SP55) protein.
 XX
 KW Sheep; group B beta-haemolytic Streptococci toxin receptor; GBS; SP55;
 KW cytosolic; vulnary; antiatherosclerotic; osteopathic; vasotropic;
 KW prevention; attenuation; pathoangiogenic condition; cancer; scar;
 KW wound healing; gliosis; nerve injury; chronic wound; reperfusion injury;
 KW keloid; rheumatoid arthritis; atherosclerosis; osteoarthritis; psoriasis;
 KW vaccine.
 XX
 OS Ovis sp.
 XX
 FH Key
 FT Region
 FT Location/Qualifiers
 FT /label= p55a_immunogenic_peptide
 FT /note= "Fragment of extracellular domain of GBS toxin
 FT receptor"
 FT 8..22
 FT 9..35
 FT /label= p56a_immunogenic_peptide
 FT 14..19
 FT /note= "Region of high hydrophilicity"
 FT 25..30
 FT /note= "Region of high hydrophilicity"
 FT 71..84
 FT /label= p57a_immunogenic_peptide
 FT /note= "Fragment of intracellular domain of GBS toxin
 FT receptor"
 FT 75..80
 FT /note= "Region of high hydrophilicity"
 FT
 FT Region
 FT WO200156598-A2.
 XX
 PN 09-AUG-2001.
 XX
 PD 02-FEB-2001; 2001WO-US003662.
 XX
 PF 02-FEB-2000; 2000US-0179870P.
 XX
 PR (UYVA-) UNIV VANDERBILT.
 XX
 PA Hellerqvist CG;
 XX
 PI WPI; 2001-488844/53.
 DR N-PSDB; AAD10326.
 XX
 DR Preventing or attenuating pathoangiogenic conditions e.g. cancer, chronic
 FT wounds, osteoarthritis, keloids and psoriasis in a mammal, by
 PT administering group B beta-haemolytic Streptococci toxin receptor or its
 PT fragment.
 XX
 PS Claim 8; Page 50-52; 52pp; English.
 XX
 CC The present sequence is group B beta-haemolytic Streptococci (GBS) toxin
 CC receptor protein, SP55 from sheep. The present invention relates to a
 CC method for preventing or attenuating a patho-angiogenic condition in a
 CC mammal which comprises administering to the mammal one or more GBS toxin
 CC receptors or their immunogenic fragments to induce or maintain an immune
 CC response to one of GBS toxin receptors. The method is useful for
 CC preventing or ameliorating pathoangiogenic conditions such as cancer,
 CC scarring during wound healing, gliosis during repair of nerve injury,
 CC chronic wounds, keloids, reperfusion injury, rheumatoid arthritis,
 CC atherosclerosis, osteoarthritis and psoriasis in mammals. The proteins of
 CC the invention are also used as vaccines
 CC
 SQ Sequence 495 AA;
 Query Match 82.1%; Score 2329; DB 4; Length 495;

QY 128 SARIKHHNQTGKKYQWDAETQGMILGSPFYGYITITQPGYVASKIGKMLGFGILGT 187
 CC 126 SARIKHHNQTGKKYQWDAETQGMILGSPFYGYITITQPGYVASKIGKMLGFGILGT 185
 Db 188 AVITLFTPIAADGVGPIVLRLALEGEGVTFPAMAMMSWAPLERSKLISISYAGA 247
 QY 186 AVITLFTPIAADGVGPIVLRLALEGEGVTFPAMAMMSWAPLERSKLISISYAGA 245
 Db 248 QLGTVISLPLSGIICYYMMNTYVYFFGTGIFWFLMLWVSDTPQKHRIKSHYEKEYI 307
 QY 246 QLGTVISLPLSGIICYYMMNTYVYFFGTGIFWFLMLWVSDTPQKHRIKSHYEKEYI 305
 QY 308 LSSL 311
 Db 306 LSSL 309

RESULT 14
 ABP41345
 ID ABP41345 standard; protein; 284 AA.
 XX AC ABP41345;
 XX DT 22-AUG-2002 (first entry)
 XX DE Human ovarian antigen HMWCG79, SEQ ID NO:2477.
 XX Human ovarian antigen HMWCG79, SEQ ID NO:2477.
 XX Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
 KM ovarian cancer; breast cancer; tumour; reproductive system disorder;
 KM infertility; pregnancy disorders; anovulation; polycystic ovary syndrome;
 KM PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
 KM inflammatory condition; immune disorder; blood disorder;
 KM cardiovascular disorder; respiratory disorder; neurological disorder;
 KM gastrointestinal disorder; urinary system disorder; drug screening;
 KM gene therapy; chromosome mapping; forensic analysis;
 KM antibody preparation; cytostatic; immunomodulatory; neuroprotective;
 KM antiinflammatory; gynaecological; reproductive.
 XX OS Homo sapiens.
 XX PN WO200200677-A1.
 XX PD 03-JAN-2002.
 XX PF 07-JUN-2001; 2001WO-US018569.
 XX PR 07-JUN-2000; 2000US-0209467P.
 XX PA (HUMA-) HUMAN GENOME SCI INC.
 XX PI Birse CE, Rosen CA;
 XX DR MPI, 2002-147878/19.
 XX DR N-PSDB; AB054422.
 XX PT Isolated nucleic acid molecules encoding novel ovarian polypeptides,
 PT useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian
 PT cancer), immune disorders, cardiovascular disorders and neurological
 PT diseases.
 XX PS Claim 11; SEQ ID NO 2477; 2922pp; English.

CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
 CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine
 CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
 CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
 CC vaginitis), immune disorders (e.g., congenital and acquired
 CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
 CC blood-related disorders (e.g., anaemia), cardiovascular disorders,
 CC respiratory disorders, neurological disorders, gastrointestinal disorders
 CC and urinary system disorders. Ovarian antigen polypeptides and
 CC polynucleotides may also be used in screening for compounds which
 CC modulate ovarian antigen expression or activity. The polynucleotides may
 CC further be used for gene therapy, chromosome mapping, in the
 CC identification of individuals and in forensic analysis, and the
 CC polypeptides may be used as food additives or to prepare antibodies
 CC useful in disease diagnosis, drug targeting and phenotyping. The present
 CC sequence represents a human ovarian antigen of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 284 AA;

Query Match 53.6%; Score 1521; DB 5; Length 284;
 Best Local Similarity 100.0%; Pred. No. 2e-147;
 Matches 284; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 253 ISPLSGIICYYMMNTYVYFFGTGIFWFLMLWVSDTPQKHRIKSHYEKEYISSLR 312
 Db 1 ISPLSGIICYYMMNTYVYFFGTGIFWFLMLWVSDTPQKHRIKSHYEKEYISSLR 60

QY 313 NOLSSQKSVBWDILKSLPMAIVAHFSYNTFTYLLTLPYMKELRFNVQENGFLS 372
 Db 61 NOLSSQKSVBWDILKSLPMAIVAHFSYNTFTYLLTLPYMKELRFNVQENGFLS 120

QY 373 SLPLSGWLCMIISGQADNLRKKNPSTLCVRIRISLIGMGPAFLVAAGFTGCDYSL 432
 Db 121 SLPLSGWLCMIISGQADNLRKKNPSTLCVRIRISLIGMGPAFLVAAGFTGCDYSL 180

QY 433 AVAFPLTISTTLGGFCSSGSFINHLDIAPSYAGILGITNFTATPGWGVFIKSLTPDN 492
 Db 181 AVAFPLTISTTLGGFCSSGSFINHLDIAPSYAGILGITNFTATPGWGVFIKSLTPDN 240

QY 493 TVGEMQTVFYIAAIVFGAIFFTLPAKGEVQWALNDHGHRRH 536
 Db 241 TVGEMQTVFYIAAIVFGAIFFTLPAKGEVQWALNDHGHRRH 284

RESULT 15
 ABB89975
 ID ABB89975 standard; protein; 272 AA.
 XX AC ABB89975;
 XX DT 24-MAY-2002 (first entry)
 XX DE Human polypeptide SEQ ID NO 2351.
 XX Cytostatic; immunosuppressive; nocrotropic; neuroprotective; antiviral;
 KM antiallergic; hepatotropic; antidiabetic; antiinflammatory; anticancer;
 KM vulnerrant; anticonvulsant; antibacterial; antifungal; antiparasitic;
 KM cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
 KM neurological disease; infection; human; secreted protein.
 XX OS Homo sapiens.
 XX PN WO200190304-A2.
 XX PD 29-NOV-2001.
 XX PF 18-MAY-2001; 2001WO-US016450.
 XX PR 19-MAY-2000; 2000US-0205515P.

PA (HUMA-) HUMAN GENOME SCI INC.

XX Birse CE, Rosen CA,

XX WPI; 2002-122018/16.

DR N-PSDB; ABL90384.

XX Novel 1405 isolated polypeptides, useful for diagnosis, treatment and
PT prevention of neural, immune system, muscular, reproductive
PT gastrointestinal, pulmonary, cardiovascular, renal and proliferative
PT disorders.

PS Claim 11; SEQ ID NO 2351; 2081bp + Sequence Listing; English.

XX
CC The invention relates to novel genes (ABL99449-ABL90853) and proteins
CC (AB99440-AB99444) useful for preventing, treating or ameliorating
CC medical conditions e.g. by protein or gene therapy. The genes are
CC isolated from a range of human tissues disclosed in the specification.
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in
CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
CC cardiovascular disorders such as myocardial ischaemias; (d) wound healing
CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
CC infectious diseases such as viral, bacterial, fungal and parasitic
CC infections. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX
SQ Sequence 272 AA;

Query Match 51.2%; Score 1451; DB 5; Length 272;

Best Local Similarity 99.6%; Pred. No. 3e-140;

Matches 271; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 265 MNWTVYVFYFCTTIGIFWFLMIWLVSDTPQKHRIKSHYEKEYIISLRLNQLSSQKSVPMV 324

DB 1 MNWTVYVFYFCTTIGIFWFLMIWLVSDTPQKHRIKSHYEKEYIISLRLNQLSSQKSVPMV 60

QY 325 PILKSLPLMAIVVAHFSYNTFTYLLTLPTMKEILRFNVQENGFLSSLPYLGSWLCMI 384

DB 61 PILKSLPLMAIVVAHFSYNTFTYLLTLPTMKEILRFNVQENGFLSSLPYLGSWLCMI 120

QY 385 LSGQPADNLRKKNFSTLCVRRIFSLIGMIGPAVFLVAAGFIGCDYSLAVAFITISTLG 444

DB 121 LSGQPADNLRKKNFSTLCVRRIFSLIGMIGPAVFLVAAGFIGCDYSLAVAFITISTLG 180

QY 445 GFCSGSGSINHLDIAPSYAGILGITNTFATIPGMNGPVIKSLTPDNTVGEMQTVFYIA 504

DB 181 GFCSGSGSINHLDIAPSYAGILGITNTFATIPGMNGPVIKSLTPDNTVGEMQTVFYIA 240

QY 505 AAINVFGAIFFTLLFAKGEVQWMAINDHGHHRH 536

DB 241 AAINVFGAIFFTLLFAKGEVQWMAINDHGHHRH 272

Search completed: June 7, 2006, 05:37:46

Job time : 201 secs

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November 2005

Published_Applications_Nucleic Acid and Published_Applications_Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New).

Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

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GenCore version 5.1.9
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OM protein - protein search, using SW model

Run on: June 7, 2006, 05:43:57 ; Search time 188 Seconds
(without alignments)
1320.655 Million cell updates/sec

Title: US-10-823-506-8

Perfect score: 2836

Sequence: 1 MAGAMTPPRPVQPARPGCF.....LFAKGEVQWALNDHHGRH 536

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications_AA_Main:
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5: /EMC_Celerra_SIDS3/prodata/2/pubppaa/US10_PUBCOMB.pep.*
6: /EMC_Celerra_SIDS3/prodata/2/pubppaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2836	100.0	536	3 US-09-776-865-2	Sequence 2, Appl1
2	2836	100.0	536	5 US-10-823-506-8	Sequence 8, Appl1
3	2621	92.4	495	5 US-09-915-181A-7	Sequence 7, Appl1
4	2621	92.4	495	4 US-10-755-889-588	Sequence 588, App
5	2621	92.4	495	5 US-10-823-506-2	Sequence 2, Appl1
6	2621	92.4	495	5 US-10-631-467-768	Sequence 768, App
7	2329	82.1	495	3 US-09-776-865-4	Sequence 4, Appl1
8	2329	82.1	495	5 US-10-823-506-4	Sequence 4, Appl1
9	1698	59.9	495	5 US-10-823-506-10	Sequence 10, Appl1
10	1698	59.9	495	5 US-10-823-506-12	Sequence 12, Appl1
11	1521	53.6	284	4 US-10-264-049-2477	Sequence 2477, Ap
12	1451	51.2	272	4 US-10-264-237-2351	Sequence 2351, Ap
13	996.5	35.1	559	6 US-11-097-143-2895	Sequence 2895, Ap
14	992	35.0	502	6 US-11-097-143-8367	Sequence 8367, Ap
15	992	35.0	502	6 US-11-097-143-24411	Sequence 24411, A
16	987	34.8	493	4 US-10-369-493-5834	Sequence 5834, Ap
17	970	34.2	578	3 US-09-740-041-4	Sequence 4, Appl1
18	970	34.2	578	4 US-10-389-967-4	Sequence 4, Appl1
19	970	34.2	582	3 US-09-915-181A-4	Sequence 4, Appl1
20	970	34.2	582	4 US-10-205-331-7	Sequence 4, Appl1
21	970	34.2	582	5 US-10-734-731-12	Sequence 12, Appl1
22	970	34.2	582	5 US-10-734-731-14	Sequence 14, Appl1
23	970	34.2	582	5 US-10-807-500-12	Sequence 12, Appl1
24	970	34.2	582	5 US-10-807-500-14	Sequence 14, Appl1
25	965.5	34.0	582	5 US-10-734-731-10	Sequence 10, Appl1
26	965.5	34.0	582	5 US-10-807-500-10	Sequence 10, Appl1
27	955	33.7	589	3 US-09-740-041-2	Sequence 2, Appl1

28	955	33.7	589	4 US-10-389-967-2	Sequence 2, Appl1
29	955	33.7	589	5 US-10-499-731-28	Sequence 28, Appl1
30	945	33.3	601	5 US-10-499-731-46	Sequence 46, Appl1
31	941	33.2	560	5 US-10-734-731-2	Sequence 2, Appl1
32	941	33.2	560	5 US-10-807-500-2	Sequence 2, Appl1
33	941	33.2	560	5 US-10-756-149-5598	Sequence 5598, Ap
34	940.5	33.2	566	4 US-10-287-226-300	Sequence 300, App
35	940	33.1	560	4 US-10-314-790-5	GENERAL INFORMA
36	940	33.1	560	5 US-10-734-731-4	Sequence 4, Appl1
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38	939	33.1	1294	4 US-10-286-115-1200	Sequence 1200, Ap
39	936	33.0	560	3 US-09-991-212A-4	Sequence 4, Appl1
40	936	33.0	560	3 US-09-915-181A-5	Sequence 5, Appl1
41	936	33.0	560	3 US-09-965-522-4	Sequence 4, Appl1
42	936	33.0	560	5 US-10-734-731-6	Sequence 6, Appl1
43	936	33.0	560	5 US-10-734-731-8	Sequence 8, Appl1
44	936	33.0	560	5 US-10-807-500-6	Sequence 6, Appl1
45	936	33.0	560	5 US-10-807-500-8	Sequence 8, Appl1

ALIGNMENTS

RESULT 1					
US-09-776-865-2					
; Sequence 2, Application US/09776865					
; Patent No. US20020061846A1					
; GENERAL INFORMATION:					
; APPLICANT: Hellerqvist, Carl					
; TITLE OF INVENTION: Methods for Preventing or Attenuating Pathoangiogenic Conditions					
; FILE REFERENCE: 22100-0100 46126-252687					
; CURRENT APPLICATION NUMBER: US/09/776,865					
; CURRENT FILING DATE: 2001-02-02					
; PRIOR APPLICATION NUMBER: US 60/179,870					
; PRIOR FILING DATE: 2000-02-02					
; NUMBER OF SEQ ID NOS: 4					
; SOFTWARE: PatentIn version 3.0					
; SEQ ID NO 2					
; LENGTH: 536					
; TYPE: PRT					
; ORGANISM: Homo sapiens					
; US-09-776-865-2					
Query Match 100.0%; Score 2836; DB 3; Length 536;					
Best Local Similarity 100.0%; Pred. No. 4.3e-249;					
Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
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DB	1	MAAGMT	PPRPVQPARPGFGLSGRRSLCQVASTPAHVGWMS	PVRDLARNDGEESTDR	60
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DB	61	TLPLPGAPRAEAP	VCSCARSYNLAIIAFRGFFIVYALRVNL	SYALVDMVDSNTTLEENRT	120
QY	121	SKACPEHSAP	IKYHNHNOTGKKYQWDAETQGMISGFYGIITQIPGGYAS	KIGGKML	180
DB	121	SKACPEHSAP	IKYHNHNOTGKKYQWDAETQGMISGFYGIITQIPGGYAS	KIGGKML	180
QY	181	GFGILGTAVLT	LTPTPIADIGVPLILVRLAEGAGGVTPRANHAMWS	SAAPPLERSKLL	240
DB	181	GFGILGTAVLT	LTPTPIADIGVPLILVRLAEGAGGVTPRANHAMWS	SAAPPLERSKLL	240
QY	241	SISYAGAGTGT	IVSLPSGIICYNNMTYVFYFGTIGFWLLMTLWLS	VDTPQKHRS	300
DB	241	SISYAGAGTGT	IVSLPSGIICYNNMTYVFYFGTIGFWLLMTLWLS	VDTPQKHRS	300
QY	301	HYEKEYILSL	RLQSSOKSVPMVPLTKSLPLMAIVVAHSYVMFTYTLTL	LPYWKEL	360
DB	301	HYEKEYILSL	RLQSSOKSVPMVPLTKSLPLMAIVVAHSYVMFTYTLTL	LPYWKEL	360
QY	361	LRENVQENGL	SLSPYLGWLCMILSGOADNLRANKNFSTLCVRRIFSLIGM	IGAVFL	420
DB	361	LRENVQENGL	SLSPYLGWLCMILSGOADNLRANKNFSTLCVRRIFSLIGM	IGAVFL	420

Db 361 LRFNVQENGFLSSLPLVGSWLCMLISGOAADNLRAKNFSTLCVRRIFFSLIGMIGPAVFL 420

Qy 421 VAAFGICDYSLAVAFLLTSTTGGFCSSGFSINHLDIASVAGILLGINTPATTPGMV 480

Db 422 VAAFGICDYSLAVAFLLTSTTGGFCSSGFSINHLDIASVAGILLGINTPATTPGMV 480

Qy 481 GPVIAKSLTPDNTVGEQVTFYIAAAINVGAIFFTLFAKGEVQNMALNDHGHRRH 536

Db 481 GPVIAKSLTPDNTVGEQVTFYIAAAINVGAIFFTLFAKGEVQNMALNDHGHRRH 536

RESULT 2

US-10-823-506-8

Sequence 8, Application US/10823506

Publication No. US20050002931A1

GENERAL INFORMATION:

APPLICANT: Heileqvist, Carl

APPLICANT: Fu, Changlin

TITLE OF INVENTION: GBS Toxin Receptor

FILE REFERENCE: CARB-008/01US

CURRENT APPLICATION NUMBER: US/10/823,506

CURRENT FILING DATE: 2004-04-12

PRIOR APPLICATION NUMBER: US/09/359,167

PRIOR FILING DATE: 1999-07-21

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60-693,843

PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-22

NUMBER OF SEQ ID NOS: 12

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 8

LENGTH: 536

TYPE: PR

ORGANISM: Homo sapiens

US-10-823-506-8

Query Match 100.0%; Score 2836; DB 5; Length 536;

Best Local Similarity 100.0%; Pred. No. 4,3e-249;

Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAAGANTPPRPVQPARPGFGLSGRRSLLCQVASTPAHVGMSPVVDLARNDEESTDR 60

Db 1 MAAGANTPPRPVQPARPGFGLSGRRSLLCQVASTPAHVGMSPVVDLARNDEESTDR 60

Qy 61 TPLPGAPRAEAPVCCSARYNLAITLAFGFFIYVALRVNLVVALVMDVSDNTLLEDRNT 120

Db 61 TPLPGAPRAEAPVCCSARYNLAITLAFGFFIYVALRVNLVVALVMDVSDNTLLEDRNT 120

Qy 121 SKACPEHSAPIKVHNQTKKKYQWDAETQGMILGSFFYGYITTOIPGYYASKIGKMLL 180

Db 121 SKACPEHSAPIKVHNQTKKKYQWDAETQGMILGSFFYGYITTOIPGYYASKIGKMLL 180

Qy 181 GFGILGAVLTLPPIADIGVGPLIVLRALLEGEGEVTPPAMAMMSMAPLERSKLL 240

Db 181 GFGILGAVLTLPPIADIGVGPLIVLRALLEGEGEVTPPAMAMMSMAPLERSKLL 240

Qy 241 SISYAGQLGTIVSLPLSGIICYYMMNTYVFFFGTIGIFWFLIMVLVSDTPQKHRRIS 300

Db 241 SISYAGQLGTIVSLPLSGIICYYMMNTYVFFFGTIGIFWFLIMVLVSDTPQKHRRIS 300

Qy 301 HYEKEYTLSSLRNQLSSQKSVPMVPIIKSLPLMAIVVAHFSYNNFTYLLTLFTYKKEI 360

Db 301 HYEKEYTLSSLRNQLSSQKSVPMVPIIKSLPLMAIVVAHFSYNNFTYLLTLFTYKKEI 360

Qy 361 LRFNVQENGFLSSLPLVGSWLCMLISGOAADNLRAKNFSTLCVRRIFFSLIGMIGPAVFL 420

Db 361 LRFNVQENGFLSSLPLVGSWLCMLISGOAADNLRAKNFSTLCVRRIFFSLIGMIGPAVFL 420

Qy 421 VAAFGICDYSLAVAFLLTSTTGGFCSSGFSINHLDIASVAGILLGINTPATTPGMV 480

Db 421 VAAFGICDYSLAVAFLLTSTTGGFCSSGFSINHLDIASVAGILLGINTPATTPGMV 480

Qy 481 GPVIAKSLTPDNTVGEQVTFYIAAAINVGAIFFTLFAKGEVQNMALNDHGHRRH 536

Db 481 GPVIAKSLTPDNTVGEQVTFYIAAAINVGAIFFTLFAKGEVQNMALNDHGHRRH 536

RESULT 3

US-09-915-181A-7

Sequence 7, Application US/09915181A

Patent No. US20020098473A1

GENERAL INFORMATION:

APPLICANT: EDWARDS, ROBERT

APPLICANT: BELLOCCHIO, ELIZABETH

APPLICANT: FREMEAUX, ROBERT

APPLICANT: REIMER, RICHARD

TITLE OF INVENTION: NOVEL GLUTAMATE TRANSPORTERS

FILE REFERENCE: 305T-932610US

CURRENT APPLICATION NUMBER: US/09/915,181A

CURRENT FILING DATE: 2002-03-26

PRIOR APPLICATION NUMBER: US 60/220,556

PRIOR FILING DATE: 2000-07-25

NUMBER OF SEQ ID NOS: 11

SOFTWARE: PatentIn version 3.0

SEQ ID NO 7

LENGTH: 495

TYPE: PR

ORGANISM: Homo sapiens

US-09-915-181A-7

Query Match 92.4%; Score 2621; DB 3; Length 495;

Best Local Similarity 100.0%; Pred. No. 1,5e-229;

Matches 495; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 42 MRSVPDLARNDEESTDRTPPLPGAPRAEAPVCCSARYNLAITLAFGFFIYVALRVNL 101

Db 1 MRSVPDLARNDEESTDRTPPLPGAPRAEAPVCCSARYNLAITLAFGFFIYVALRVNL 101

Qy 102 SVLVVMDVSDNTLLEDRNTSKACPEHSAPIKVHNQTKKKYQWDAETQGMILGSFFYGYI 161

Db 102 SVLVVMDVSDNTLLEDRNTSKACPEHSAPIKVHNQTKKKYQWDAETQGMILGSFFYGYI 161

Qy 162 ITTOIPGYYASKIGKMLLFGILGAVLTLPPIADIGVGPLIVLRALLEGEGEVTPP 221

Db 162 ITTOIPGYYASKIGKMLLFGILGAVLTLPPIADIGVGPLIVLRALLEGEGEVTPP 221

Qy 222 AMHAMSSMAPLERSKLLSISYAGQLGTIVSLPLSGIICYYMMNTYVFFFGTIGIFW 281

Db 222 AMHAMSSMAPLERSKLLSISYAGQLGTIVSLPLSGIICYYMMNTYVFFFGTIGIFW 281

Qy 282 FLIMVLVSDTPQKHRRISHYEKEYTLSSLRNQLSSQKSVPMVPIIKSLPLMAIVVAHFS 341

Db 282 FLIMVLVSDTPQKHRRISHYEKEYTLSSLRNQLSSQKSVPMVPIIKSLPLMAIVVAHFS 341

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Qy 522 EVQNMALNDHGHRRH 536

Db 522 EVQNMALNDHGHRRH 536

RESULT 4

US-10-755-889-588

Sequence 588, Application US/10755889

Publication No. US20040171823A1

GENERAL INFORMATION:

APPLICANT: Bristol-Myers Squibb Company

TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-KB

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; TITLE OF INVENTION: PATHWAY
; FILE REFERENCE: D0284 NP
; CURRENT APPLICATION NUMBER: US/10/755,889
; CURRENT FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: U.S. 60/440,068
; PRIOR FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: U.S. 60/469,757
; PRIOR FILING DATE: 2003-05-12
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 588
; LENGTH: 495
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-755-889-588

Query Match          92.4%; Score 2621; DB 4; Length 495;
Best Local Similarity 100.0%; Pred. No. 1.5e-229;
Matches 495; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 102 SVALVDMVDSNTTLEDRNRTSKACPEHSAPIKVHNHNOTGKRYQMDAETQGMILGSFFGYI 161
DB 61 SVALVDMVDSNTTLEDRNRTSKACPEHSAPIKVHNHNOTGKRYQMDAETQGMILGSFFGYI 120
QY 162 ITQIPGGYVASKIGKMLGFGILGTVLTLFTPIAADLGVPPLIVRALEGEGVTFP 221
DB 121 ITQIPGGYVASKIGKMLGFGILGTVLTLFTPIAADLGVPPLIVRALEGEGVTFP 180
QY 222 AMHAMSSMAPPLERSKULSISYAGQLGTVISLPSGII CYNNMTYVYFFGTIGIFW 281
DB 181 AMHAMSSMAPPLERSKULSISYAGQLGTVISLPSGII CYNNMTYVYFFGTIGIFW 240
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DB 241 FLIMIMLVSDTPQKHRIKSHYEKEYILSLRNQSSQKSPWVPILKSLPLMAIVAHFS 300
QY 342 YNNTFYTLTLPTMYKEILRFNVQENGFLSSLPYGSWLCMILSGQAADNLRAKNMFST 401
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QY 402 LCVRRIFSLIGMIGPAVFLVAAGFIGDYSIAVAFLTISTLLGFCSSGSGSINHLDIAPS 461
DB 361 LCVRRIFSLIGMIGPAVFLVAAGFIGDYSIAVAFLTISTLLGFCSSGSGSINHLDIAPS 420
QY 462 YAGILGINTTPTATIPGMGVPVIAKSLTPNTVGENQTVFYIAAINVFGAIFFTLPAGK 521
DB 421 YAGILGINTTPTATIPGMGVPVIAKSLTPNTVGENQTVFYIAAINVFGAIFFTLPAGK 480
QY 522 EVONMALNDHGHGRH 536
DB 481 EVONMALNDHGHGRH 495

RESULT 5
US-10-823-506-2
; Sequence 2, Application US/10823506
; Publication No. US20050002931A1
; GENERAL INFORMATION:
; APPLICANT: Hellerqvist, Carl
; APPLICANT: Fu, Changlin
; TITLE OF INVENTION: GBS Toxin Receptor
; FILE REFERENCE: CARB-008/01US
; CURRENT APPLICATION NUMBER: US/10/823,506
; CURRENT FILING DATE: 2004-04-12
; PRIOR APPLICATION NUMBER: US/09/359,167
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60-693,843
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-22
; NUMBER OF SEQ ID NOS: 12
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 495
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-823-506-2

Query Match          92.4%; Score 2621; DB 5; Length 495;
Best Local Similarity 100.0%; Pred. No. 1.5e-229;
Matches 495; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 MRSPPVDLARNDEESTDRTPLLPGAPRAEAPVCCSARYNLAILAFFGFYVYALRVNL 101
DB 1 MRSPPVDLARNDEESTDRTPLLPGAPRAEAPVCCSARYNLAILAFFGFYVYALRVNL 60
QY 102 SVALVDMVDSNTTLEDRNRTSKACPEHSAPIKVHNHNOTGKRYQMDAETQGMILGSFFGYI 161
DB 61 SVALVDMVDSNTTLEDRNRTSKACPEHSAPIKVHNHNOTGKRYQMDAETQGMILGSFFGYI 120
QY 162 ITQIPGGYVASKIGKMLGFGILGTVLTLFTPIAADLGVPPLIVRALEGEGVTFP 221
DB 121 ITQIPGGYVASKIGKMLGFGILGTVLTLFTPIAADLGVPPLIVRALEGEGVTFP 180
QY 222 AMHAMSSMAPPLERSKULSISYAGQLGTVISLPSGII CYNNMTYVYFFGTIGIFW 281
DB 181 AMHAMSSMAPPLERSKULSISYAGQLGTVISLPSGII CYNNMTYVYFFGTIGIFW 240
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DB 241 FLIMIMLVSDTPQKHRIKSHYEKEYILSLRNQSSQKSPWVPILKSLPLMAIVAHFS 300
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DB 301 YNNTFYTLTLPTMYKEILRFNVQENGFLSSLPYGSWLCMILSGQAADNLRAKNMFST 360
QY 402 LCVRRIFSLIGMIGPAVFLVAAGFIGDYSIAVAFLTISTLLGFCSSGSGSINHLDIAPS 461
DB 361 LCVRRIFSLIGMIGPAVFLVAAGFIGDYSIAVAFLTISTLLGFCSSGSGSINHLDIAPS 420
QY 462 YAGILGINTTPTATIPGMGVPVIAKSLTPNTVGENQTVFYIAAINVFGAIFFTLPAGK 521
DB 421 YAGILGINTTPTATIPGMGVPVIAKSLTPNTVGENQTVFYIAAINVFGAIFFTLPAGK 480
QY 522 EVONMALNDHGHGRH 536
DB 481 EVONMALNDHGHGRH 495

RESULT 6
US-10-631-467-768
; Sequence 768, Application US/10631467
; Publication No. US20050208496A1
; GENERAL INFORMATION:
; APPLICANT: Genox Research Inc.
; TITLE OF INVENTION: Method for testing for bronchial asthma, or chronic obstructive
; FILE REFERENCE: 3462.1005-000
; CURRENT APPLICATION NUMBER: US/10/631,467
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: JP 2003-077212
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: JP 2002-229312
; PRIOR FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 2086
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 768
; LENGTH: 495
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-631-467-768

Query Match          92.4%; Score 2621; DB 5; Length 495;
Best Local Similarity 100.0%; Pred. No. 1.5e-229;
```

Matches	Conservative	0	Mismatches	0	Indels	0	Gaps	0
QY	42	MRSPYRDLARNDEESTDRTPLPGAPRAEAAPVCCSARYNLALIAFFGFTIVYALRVNL	101					
Db	1	MRSPYRDLARNDEESTDRTPLPGAPRAEAAPVCCSARYNLALIAFFGFTIVYALRVNL	60					
QY	102	SVALVDWDSNTTLEDNRTSKACPEHSAPIKVHNNOTGKKYQMDAETQGMILGSPFYGYI	161					
Db	61	SVALVDWDSNTTLEDNRTSKACPEHSAPIKVHNNOTGKKYQMDAETQGMILGSPFYGYI	120					
QY	162	ITQIPGVYASIKGGKMLGFGILGTAVTLFTPIAADGVGPLYLRLAEGEGEVTPP	221					
Db	121	ITQIPGVYASIKGGKMLGFGILGTAVTLFTPIAADGVGPLYLRLAEGEGEVTPP	180					
QY	222	AMHAMSSWAPPLERSKULSISYAGAOIGTVISLPSLGIIICYYMMNTVYFYEFGTIGIPW	281					
Db	181	AMHAMSSWAPPLERSKULSISYAGAOIGTVISLPSLGIIICYYMMNTVYFYEFGTIGIPW	240					
QY	282	FLMWLWVSDTPQOKKRISHYEKEYILSLRNQDSQKSVPMVPIKSLPLMAIVVAHS	341					
Db	241	FLMWLWVSDTPQOKKRISHYEKEYILSLRNQDSQKSVPMVPIKSLPLMAIVVAHS	300					
QY	342	YNNETVTTTTLLPTMKETILRFNVOENGSLSPYIGSLCMILSGOADDNLRAKNFST	401					
Db	301	YNNETVTTTTLLPTMKETILRFNVOENGSLSPYIGSLCMILSGOADDNLRAKNFST	360					
QY	402	LCVRRIFSLIGMIGPAVFLVAAGFTGCDYSLAVAFLLITSTLLGFCSSGFSINHLDIAPS	461					
Db	361	LCVRRIFSLIGMIGPAVFLVAAGFTGCDYSLAVAFLLITSTLLGFCSSGFSINHLDIAPS	420					
QY	462	YAGILGTTNTTATIPGMVGPVIAKSLTPDNTVGEQVTFYIAAAINVGALFPTLPAG	521					
Db	421	YAGILGTTNTTATIPGMVGPVIAKSLTPDNTVGEQVTFYIAAAINVGALFPTLPAG	480					
QY	522	EYQNNALNDHHGHRH	536					
Db	481	EYQNNALNDHHGHRH	495					
RESULT 7								
US-09-776-865-4								
; Sequence 4, Application US/09776865								
; Patent No. US2002061846A1								
; GENERAL INFORMATION:								
; APPLICANT: Hellerqvist, Carl								
; TITLE OF INVENTION: Methods for Preventing or Attenuating Pathoangiogetic Conditions								
; FILE REFERENCE: 22100-0100 46126-252687								
; CURRENT FILING DATE: 2001-02-02								
; PRIOR APPLICATION NUMBER: US 60/179, 870								
; PRIOR FILING DATE: 2000-02-02								
; NUMBER OF SEQ ID NOS: 4								
; SOFTWARE: PatentIn version 3.0								
; SEQ ID NO 4								
; LENGTH: 495								
; TYPE: PRT								
; ORGANISM: Ovis sp.								
US-09-776-865-4								
Query Match								
Best Local Similarity 82.1%; Score 2329; DB 3; Length 495;								
Matches 427; Conservative 39; Mismatches 29; Indels 0; Gaps 0;								
QY	42	MRSPYRDLARNDEESTDRTPLPGAPRAEAAPVCCSARYNLALIAFFGFTIVYALRVNL	101					
Db	1	MRSPYRDLARNDEESTDRTPLPGAPRAEAAPVCCSARYNLALIAFFGFTIVYALRVNL	60					
QY	102	SVALVDWDSNTTLEDNRTSKACPEHSAPIKVHNNOTGKKYQMDAETQGMILGSPFYGYI	161					
Db	61	SVALVDWDSNTTLEDNRTSKACPEHSAPIKVHNNOTGKKYQMDAETQGMILGSPFYGYI	120					
QY	162	ITQIPGVYASIKGGKMLGFGILGTAVTLFTPIAADGVGPLYLRLAEGEGEVTPP	221					

Db	121	ITQIPGVYVASSSGKLLGFGICFATATFTLFTPLAADGVALVALRALBGLBEGVTP	180
Qy	222	AMHAMSSWAPPLESKLISISYAGAOIGTVISLPSGICCYMMWTVYFFFGTIGFM	281
Db	181	AMHAMSSWAPPLESKLISISYAGAOIGTVISLPSGTCYMMWTVYFFFGVIGIWM	240
Qy	282	FLMTWLVSDPPOKHRIISHEKEYITLSLRNQLSQSKSVPMVPIKSLPLMAIVAAHS	341
Db	241	FLMTCLVSDPETHKTIITPYEKEYITLSLRNQLSQSKSVPMIPMLKSLPLMAIVAAHS	300
Qy	342	YNNFYYTLTLTLPTMYKEILRFNVOENGLSGLPYLGSMLCMIISGQADNLRAKNFST	401
Db	301	YNNFYYTLTLTLPTMYKEVLRNNGIENGFLSAVPLYGCLCMIISGQADNLRAKNFST	360
Qy	402	LCVRRIFSLIGMIGPAVFLVAAGFGCDYSLAVALITSTLIGGCCSGFSINHLDIAS	461
Db	361	LMVRVFLSLIGMIGPAFLVAAGFGCDYSIALVALITSTLIGGCCSGFSINHLDIAS	420
Qy	462	YAGILGIGTNPATIPGMVGPPIAKSLPDPNVGEMQVIFYIAAINVGAIFTLFAGK	521
Db	421	YAGILGIGTNPATIPGMIGPIIARSLPENTIGEMQVIFYIAAINVGAIFTLFAGK	480
Qy	522	EVQNNALNDHHGHRH	536
Db	481	EVQNNALISDHGHRN	495
RESULT 8			
US-10-823-506-4			
; Sequence 4, Application US/10823506			
; Publication No. US20050002931A1			
; GENERAL INFORMATION:			
; APPLICANT: Hellerqvist, Carl			
; APPLICANT: Fu, Changlin			
; TITLE OF INVENTION: GBS Toxin Receptor			
; FILE REFERENCE: CARB-008/01US			
; CURRENT APPLICATION NUMBER: US/10/823,506			
; CURRENT FILING DATE: 2004-04-12			
; PRIOR APPLICATION NUMBER: US/09/359,167			
; PRIOR FILING DATE: 1999-07-21			
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60-693,843			
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-22			
; NUMBER OF SEQ ID NOS: 12			
; SOFTWARE: Patentin Ver. 2.0			
; SEQ ID NO 4			
; LENGTH: 495			
; TYPE: PRT			
; ORGANISM: Ovis sp.			
US-10-823-506-4			
Query Match			
Best Local Similarity 86.1%; Score 2329; DB 5; Length 495;			
Matches 427; Conservative 39; Mismatches 29; Indels 0; Gaps 0			
Qy	42	MRSPIRLARNDGESTDRTPLLPAPRAEAPVCCSARVNLALIAFGEFIVYALRVNL	101
Db	1	MKSPVSDIAPSGDEGSDRTPLLQRAPEAPVCCSAYNNAFLSFFEFVLYSLRVNL	60
Qy	102	SVALLVDMVDSNTTLEDNRNTRKACPEHSAPIKVVHNNQGTAKYQWDAETQGMIGSFYGYI	161
Db	61	SVALLVDMVDSNTTADNDNTSYCAHSAPIKVLHNNQGTAKYQWDAETQGMIGSFYGYI	120
Qy	162	ITQIPGVYVASKIGSKMLIGFGILGTAVLTFTPLAADIGVPLVYRALBGLBEGVTP	221
Db	121	ITQIPGVYVASSGGKLLGFGICFATATFTLFTPLAADGVALVALRALBGLBEGVTP	180
Qy	222	AMHAMSSWAPPLESKLISISYAGAOIGTVISLPSGICCYMMWTVYFFFGTIGFM	281
Db	181	AMHAMSSWAPPLESKLISISYAGAOIGTVISLPSGTCYMMWTVYFFFGVIGIWM	240
Qy	282	FLMTWLVSDPPOKHRIISHEKEYITLSLRNQLSQSKSVPMVPIKSLPLMAIVAAHS	341
Db	241	FLMTCLVSDPETHKTIITPYEKEYITLSLRNQLSQSKSVPMIPMLKSLPLMAIVAAHS	300
Qy	342	YNNFYYTLTLTLPTMYKEILRFNVOENGLSGLPYLGSMLCMIISGQADNLRAKNFST	401
Db	301	YNNFYYTLTLTLPTMYKEVLRNNGIENGFLSAVPLYGCLCMIISGQADNLRAKNFST	360
Qy	402	LCVRRIFSLIGMIGPAVFLVAAGFGCDYSLAVALITSTLIGGCCSGFSINHLDIAS	461
Db	361	LMVRVFLSLIGMIGPAFLVAAGFGCDYSIALVALITSTLIGGCCSGFSINHLDIAS	420
Qy	462	YAGILGIGTNPATIPGMVGPPIAKSLPDPNVGEMQVIFYIAAINVGAIFTLFAGK	521
Db	421	YAGILGIGTNPATIPGMIGPIIARSLPENTIGEMQVIFYIAAINVGAIFTLFAGK	480
Qy	522	EVQNNALNDHHGHRH	536
Db	481	EVQNNALISDHGHRN	495
Db	241	FLMTCLVSDPETHKTIITPYEKEYITLSLRNQLSQSKSVPMIPMLKSLPLMAIVAAHS	300


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Db      481 EXQWXXXDHGHR 494

RESULT 11
US-10-264-049-2477
; Sequence 2477, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birste et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133P1
; CURRENT APPLICATION NUMBER: US/10/264,049
; PRIOR FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 2477
; LENGTH: 284
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-049-2477

Query Match      53.6%; Score 1521; DB 4; Length 284;
Best Local Similarity 100.0%; Pred. No. 1,1e-129;
Matches 284; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 253 ISLPLSGIICYYMMNTYVFYFPGTIGIFWFLMTIMLVSDTPQKHRIISHYEKEYILSLR 312
DB 1 ISLPLSGIICYYMMNTYVFYFPGTIGIFWFLMTIMLVSDTPQKHRIISHYEKEYILSLR 60

QY 313 NQSSQKSVMPVPIIKSLPLMAIIVAHFSYNTFTYLLTLPYWKELIRNVQENGFLS 372
DB 61 NQSSQKSVMPVPIIKSLPLMAIIVAHFSYNTFTYLLTLPYWKELIRNVQENGFLS 120

QY 373 SLPLGSLWLCMILSGQADNLRANKNFTSLCVRRIFSLIGMIGPAVFLVAGFTGCDYSL 432
DB 121 SLPLGSLWLCMILSGQADNLRANKNFTSLCVRRIFSLIGMIGPAVFLVAGFTGCDYSL 180

QY 433 AVAFLTISTLGGSCSGFSINHLDIAPSYAGILGINTPATIPGMVGPVIAKSLTPDN 492
DB 181 AVAFLTISTLGGSCSGFSINHLDIAPSYAGILGINTPATIPGMVGPVIAKSLTPDN 240

QY 493 TVGEMQTVFYIAAIVNFGAIFFTLFAKGEVQNMALNDHGHHRH 536
DB 241 TVGEMQTVFYIAAIVNFGAIFFTLFAKGEVQNMALNDHGHHRH 284

RESULT 12
US-10-264-237-2351
; Sequence 2351, Application US/10264237
; Publication No. US20040009491A1
; GENERAL INFORMATION:
; APPLICANT: Birste et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA131P1
; CURRENT APPLICATION NUMBER: US/10/264,237
; PRIOR FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 2351
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE

; LOCATION: (55)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-264-237-2351

Query Match      51.2%; Score 1451; DB 4; Length 272;
Best Local Similarity 99.6%; Pred. No. 2,4e-123;
Matches 271; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 265 MNMTYVFPGTIGIFWFLMTIMLVSDTPQKHRIISHYEKEYILSLRNQSSQKSVPMW 324
DB 1 MNMTYVFPGTIGIFWFLMTIMLVSDTPQKHRIISHYEKEYILSLRNQSSQKSVPMW 60

QY 325 PILKSLPLMAIIVAHFSYNTFTYLLTLPYWKELIRNVQENGFLSLPYLGSWLCMT 384
DB 61 PILKSLPLMAIIVAHFSYNTFTYLLTLPYWKELIRNVQENGFLSLPYLGSWLCMT 120

QY 385 LSGQADNLRANKNFTSLCVRRIFSLIGMIGPAVFLVAGFTGCDYSLAVAFITSTLGG 444
DB 121 LSGQADNLRANKNFTSLCVRRIFSLIGMIGPAVFLVAGFTGCDYSLAVAFITSTLGG 180

QY 445 GPCSSGFSINHLDIAPSYAGILGINTPATIPGMVGPVIAKSLTPDNVGEWQTVFYIA 504
DB 181 GPCSSGFSINHLDIAPSYAGILGINTPATIPGMVGPVIAKSLTPDNVGEWQTVFYIA 240

QY 505 AAINVFGAIFFTLFAKGEVQNMALNDHGHHRH 536
DB 241 AAINVFGAIFFTLFAKGEVQNMALNDHGHHRH 272

RESULT 13
US-11-097-143-2895
; Sequence 2895, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; PRIOR FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FaestSeq for Windows Version 4.0
; SEQ ID NO 2895
; LENGTH: 559
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-2895

Query Match      35.1%; Score 996.5; DB 6; Length 559;
Best Local Similarity 39.8%; Pred. No. 1,6e-81;
Matches 208; Conservative 91; Mismatches 171; Indels 53; Gaps 10;

QY 51 RNDEESTDR-----TPLLPGAPRAEAPVVC-CSARYNLALIAFGFPVIVLRYNLS 102
DB 31 RSDDEADDERAFCGGERPLIRSSGAABENHGCOPKTRHIFGMGFLGFAVVYAMRVNLS 90
```

QY 103 VALDMDV-----SNTLEDNRITSKACPEHSAPIKVHHN-----QTGKKYQMDAETQG 150
 Db 91 VAIVAMVQTAIPHNSNSVIDPDT---CP-LPAF---HHNSDPRPQKEGGEVWBEAIOG 143
 QY 151 WILSPFFGIIITQIPGVASKIGKMLGFGILGTAVLTFPIAADLGVPLIVRA 210
 Db 144 LVLSFFGYVLTQVPGGRMAELYGCKIYGVGLITAVFTLITPLAAMDLPLILVRI 203
 QY 211 LEGGEGVTPPAMAMSSMAPLERSKLISYVAGDQGLYISPLSGIIC---YNNW 267
 Db 204 LEGGEGVTPPAMAMSSMAPLERSKLISYVAGDQGLYISPLSGIIC---YNNW 263
 QY 268 TYVYFFGTIGIFWELMWIVSDTPQKHRIHYEKEYIISLRNQ----- 314
 Db 264 PSAFYIFGLGLIMFIAMWIVYDKSDHPRISEERVIERSLQVGLINDLAABEE 323
 QY 315 -----LSQKSVPVVPLIKSLPLMAIVAHFVYMTFTLTLPTWKEILRPV 365
 Db 324 EGOGEVSLRAPPREERIPIWSLSLTSPVLAIIITQCGQMAFYQTLETPTYSNIHFDI 383
 QY 366 QENGFLSLPYIGSLCMLISGOADNLRKKNFSTLCVRRIFSLIGMIGPAVFLVAGF 425
 Db 384 QSNMLNAVPYLTSPFVGIACSLADWMLARYISLNSYKLMNTVASVPSLIGIITY 443
 QY 426 ICGDYSIAVAFLTITSTLIGFCSSGFSINHLDIAPSVAGIILGTINTFATTIGMWGP-VI 484
 Db 444 VCGMWVMTFPLAGVSGFAGVAGNQNQHIALSRVAGTMYGITSNAANIGFLAPYI 503
 QY 485 AKSLTPDNTGEMQTVFYIAAIVFGAIFFTLPAKEGVONWA 527
 Db 504 GLIINHRETLQWHLVFWLAAGLNIAGNFYILIFASAEQGSWS 546

RESULT 14
 US-11-097-143-8367
 ; Sequence 8367, Application US/11097143
 ; Publication No. US20050208558A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Venter, J. Craig
 ; APPLICANT: et al.
 ; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
 ; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
 ; FILE REFERENCE: CLO00728
 ; CURRENT APPLICATION NUMBER: US/11/097,143
 ; CURRENT FILING DATE: 2005-04-04
 ; PRIOR APPLICATION NUMBER: 60/157,832
 ; PRIOR FILING DATE: 1999-10-05
 ; PRIOR APPLICATION NUMBER: 60/160,191
 ; PRIOR FILING DATE: 1999-10-19
 ; PRIOR APPLICATION NUMBER: 60/161,932
 ; PRIOR FILING DATE: 1999-10-28
 ; PRIOR APPLICATION NUMBER: 60/164,769
 ; PRIOR FILING DATE: 1999-11-12
 ; PRIOR APPLICATION NUMBER: 60/173,383
 ; PRIOR FILING DATE: 1999-12-28
 ; PRIOR APPLICATION NUMBER: 60/175,693
 ; PRIOR FILING DATE: 2000-01-12
 ; PRIOR APPLICATION NUMBER: 60/184,831
 ; PRIOR FILING DATE: 2000-02-24
 ; PRIOR APPLICATION NUMBER: 60/191,637
 ; PRIOR FILING DATE: 2000-03-23
 ; NUMBER OF SEQ ID NOS: 43008
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 8367
 ; LENGTH: 502
 ; TYPE: PRT
 ; ORGANISM: DROSOPHILA
 US-11-097-143-8367
 Query Match 35.0%; Score 992; DB 6; Length 502;
 Best Local Similarity 42.4%; Pred. No. 3.5e-81;

Matches 190; Conservative 93; Mismatches 149; Indels 16; Gaps 3;
 QY 80 RYNLAIAFPGFYIALRVNLASVALDMDVSNNTLEDNRITSKACPEHSAPIKVHHNQTG 139
 Db 38 RYIVVLAFFGFENVYISLRNLASVALVAMTENVYFD-----ADGNVSYQ-- 83
 QY 140 KRYQMDAETQGMILGSPFYIITQIPGVASKIGKMLGFGILGTAVLTFPIAAD 199
 Db 84 -DFPMSKQKGLILISFPFYIITQIPGVASKIGKMLGFGILGTAVLTFPIAAD 142
 QY 200 LGVGPLIVRLLEGGEVTPPAMAMSSMAPLERSKLISYVAGDQGLYISPLSG 259
 Db 143 HSLWFLFVRRIIEGFFBEVTPPGIHAVARSPPLERSRMASIFAGVAGTIVAMPSCG 202
 QY 260 IICVYMMTVYFPGGTIGIFWELMWIVSDTPQKHRIHYEKEYIISLRNQLSQK 319
 Db 203 FLATKIGVESVYFYGIIIGVITWLVFVAGSBLDFPCKEEDYIQTITGVGSGHV 262
 QY 320 SVPVVPLIKSLPLMAIVAHFVYMTFTLTLPTWKEILRPVQENGFLSLPYLGS 379
 Db 263 KHPRAIFTSWPFALMAHSHSENMGFYTLTLQPSFLRDTLNFDLGKTGLSAVPLYAM 322
 QY 380 WLCMILSGOADNLRKKNFSTLCVRRIFSLIGMIGPAVFLVAGFICGDISLAVALFTI 439
 Db 323 GILAVSGYLDWLVQVGIWTTQVRRNFNGCAFIAQVFWMLTAYL-LDPTWSVSLTI 381
 QY 440 STTLGFCSSGFSINHLDIAPSVAGIILGTINTFATTIGMWGPVIAASLTDPDNTGEMQ 499
 Db 382 AVIGAFWMSGFANVHLDIAPQHASVLMGINTFTATTIGIVSPLTIGYVTTNQTSDWKRI 441
 QY 500 VFYIAAIVFGAIFFTLPAKEGVONWA 527
 Db 442 IFFISAGIYLVGCIVWFYCGSLQEWNA 469

RESULT 15
 US-11-097-143-24411
 ; Sequence 24411, Application US/11097143
 ; Publication No. US20050208558A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Venter, J. Craig
 ; APPLICANT: et al.
 ; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
 ; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
 ; FILE REFERENCE: CLO00728
 ; CURRENT APPLICATION NUMBER: US/11/097,143
 ; CURRENT FILING DATE: 2005-04-04
 ; PRIOR APPLICATION NUMBER: 60/157,832
 ; PRIOR FILING DATE: 1999-10-05
 ; PRIOR APPLICATION NUMBER: 60/160,191
 ; PRIOR FILING DATE: 1999-10-19
 ; PRIOR APPLICATION NUMBER: 60/161,932
 ; PRIOR FILING DATE: 1999-10-28
 ; PRIOR APPLICATION NUMBER: 60/164,769
 ; PRIOR FILING DATE: 1999-11-12
 ; PRIOR APPLICATION NUMBER: 60/173,383
 ; PRIOR FILING DATE: 1999-12-28
 ; PRIOR APPLICATION NUMBER: 60/175,693
 ; PRIOR FILING DATE: 2000-01-12
 ; PRIOR APPLICATION NUMBER: 60/184,831
 ; PRIOR FILING DATE: 2000-02-24
 ; PRIOR APPLICATION NUMBER: 60/191,637
 ; PRIOR FILING DATE: 2000-03-23
 ; NUMBER OF SEQ ID NOS: 43008
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 24411
 ; LENGTH: 502
 ; TYPE: PRT
 ; ORGANISM: DROSOPHILA
 US-11-097-143-24411
 Query Match 35.0%; Score 992; DB 6; Length 502;

Best Local Similarity 42.4%; Pred. No. 3.5e-81;
Matches 190; Conservative 93; Mismatches 149; Indels 16; Gaps 3;

```

QY      80 RYNLAIARFEGFPIVALRVNLVALVDVDSNTTLEDNRTSKACPEHSAPIKVHNQTG 139
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      38 RYIVVLLAFPGFNNVSLRVNLVAIVAMTENRTVFD-----ADGNVSYQQ-- 83
QY      140 KKYQMDAEFGQWILGSEFFGYITQIPGIVASKIGKMLGFGILGTAVLTLPPIAD 139
      :||: :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      84 -DFPMDSKOKGLILSSFFGYITLOFLGGYIGTKIGNIVFGYIGSTAILTLTPMAAS 142
QY      200 LGVGPILIVRALGELGCVTFEPAMHAWMSWAPLERSKLLSISYAGAQIGTVISLPLSG 259
      :||: :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      143 HSLMFLEFVRIIEGFEFGVTFPGIHAWMARSPLEKSRVASIAFAGNVAQTVVAMPCSG 202
QY      260 IICYYMMWTVVFFYFPGTIGIFWFLMTWLVSDTPQKHRI SHYEKEYILSLRNQLSSOK 319
      :||: :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      203 FLATKXGMBEVFVFGTIGVIWITWLVFVKAGBELDRFCSKECDYIOKTIgyvGSKHV 262
QY      320 SVPWVPLKSLPLMAIVVAHFSYNTFTYTLTLPTMKELRNVOENGFISLPLYS 379
      ||: :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      263 KHPWRAIFTSMPPYAIWASHFSEWNGFYTLTOLPSFLRDTLNFDLGKTGILSAVPYLA 322
QY      380 WLCMIISGQADNLRKWNSTLCVRIIFSLIGWIGPAVFLVAAGFIGCDYSLAVAFETI 439
      :||: :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      323 GILLAVSGYIADMLQVKGITTTQVRRNFCAGFLAQTVEMLLTAYL-LDPTWSVSLTI 381
QY      440 STTLGGFCSSGFSINHLDIAPSYAGILLGITNTFPATIPGMVGPVIAKSLTPDNTVGEWOT 499
      :||: :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      382 AVGLGAPWMSGFPAVNHLDIAQHASVLMGIGNTFPATIPGIVSPLLTGTGYVTNQTSDEMRI 441
QY      500 VFYIAAIAINFGAIFFTLFAKGEVQNNWA 527
      :||: :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
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Search completed: June 7, 2006, 05:47:51
Job time : 189 secs